

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 18:42:52 ; Search time 3294 Seconds
(without alignments)
10934.445 Million cell updates/sec

Title: US-09-600-932-1_COPY_6_836

Perfect score: 831

Sequence: 1 atgaatggcttgcattcctt.....agttcatcaagaagaaaaag 831

Scoring table: OLIGO.NUC

Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_hg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_hg_hum.*

31: em_hg_inv.*

32: em_hg_other.*

33: em_hg_mus.*

34: em_hg_pln.*

35: em_hg_rtd.*

36: em_hg_nam.*

37: em_hg_vrt.*

38: em_sy.*

39: em_hgo_hum.*

40: em_hgo_mus.*

41: em_hgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	831	100.0	1594	9	AB002631 Homo sapi
2	831	100.0	1595	6	E29008 Novel colle
3	678	81.6	1016	6	AX376032 Sequence
4	678	81.6	1016	9	AY359038 Homo sapi
5	390	46.9	141262	9	AC080033 Homo sapi
6	390	46.9	182475	2	AC023487 Homo sapi
7	149	17.9	147414	9	AC107953 Homo sapi
8	149	17.9	182475	2	AC023487 Homo sapi
9	63	7.6	767	11	U92347 Homo sapien
10	35	4.2	234922	2	AC097055 Rattus no
11	28	3.4	867	10	AB016429 Mus muscu
12	28	3.4	166900	2	AC115924 Mus muscu
13	28	3.4	22510	2	AC123656 Mus muscu
14	28	3.4	345420	2	AC131337 Mus muscu
15	26	3.1	231676	2	AC117155 Rattus no
16	26	3.1	231895	2	AC127043 Rattus no
17	26	3.1	239859	2	AC119482 Rattus no
18	26	3.1	241112	2	AC106261 Rattus no
19	26	3.1	258345	2	AC123130 Rattus no
20	23	2.8	151321	2	AC136264 Rattus no
21	22	2.6	1870	8	AF092654 Lycopersi
22	22	2.6	2060	8	AF092655 Lycopersi
23	22	2.6	121112	9	AC124319 Homo sapi
24	22	2.6	163321	2	AC128541 Homo sapi
25	22	2.6	197999	2	AC134688 Homo sapi
26	22	2.6	233566	2	AC118800 Rattus no
27	22	2.6	265067	2	AC097113 Rattus no
28	21	2.5	21	6	E29013 Novel colle
29	21	2.5	21	6	BD096386 Novel sca
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31	21	2.5	31812	8	SPUNK4
32	21	2.5	110000	2	EX572105_0
33	21	2.5	110000	2	EX572105_3
34	21	2.5	128218	2	AC121096 Mus muscu
35	21	2.5	151321	2	AC136264 Rattus no
36	21	2.5	161072	9	AL356580 Human DNA
37	21	2.5	161146	10	AC121976 Mus muscu
38	21	2.5	164611	2	AC128858 Rattus no
39	21	2.5	176982	5	AL732610 Zebrafish
40	21	2.5	192174	2	AC128248 Rattus no
41	21	2.5	206839	2	AC108244 Rattus no
42	21	2.5	216840	2	AC106609 Rattus no
43	21	2.5	240597	10	AL714017 Mouse DNA
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45	21	2.5	280815	2	AC107562 Rattus no

ALIGNMENTS

RESULT 1	AB002631	Homo sapiens mRNA for collectin 34, complete cds.	1594 bp	mrna	linear	PRI 24-JUN-1999
LOCUS	AB002631	Homo sapiens mRNA for collectin 34, complete cds.	1594 bp	mrna	linear	PRI 24-JUN-1999
DEFINITION	AB002631	Homo sapiens mRNA for collectin 34, complete cds.	1594 bp	mrna	linear	PRI 24-JUN-1999
ACCESSION	AB002631	Homo sapiens mRNA for collectin 34, complete cds.	1594 bp	mrna	linear	PRI 24-JUN-1999
VERSION	AB002631.1	GI:5162874	1594 bp	mrna	linear	PRI 24-JUN-1999
KEYWORDS	collectin 34					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	1 (sites)					
AUTHORS	Ohtani, K., Suzuki, Y., Eda, S., Kawai, T., Kase, T., Yamazaki, H., Keshi, H., Sakai, Y., Fukuh, A., Sakamoto, T. and Wakamiya, N.					
TITLE	Molecular cloning of a novel human collectin from liver (CL-L1)					

J. Biol. Chem. 274 (19), 13681-13689 (1999)
 MEDLINE 99240768
 PUBMED 10224141
 REFERENCE 2 (bases 1 to 1594)
 AUTHORS Ohtani, K.
 TITLE Direct Submission
 JOURNAL Submitted (04-APR-1997) Katsuki Ohtani, Osaka Prefectural Institute
 of Public Health, Department of Pathology, 3-69, Nakamichi 1-chome
 Higashinari-ku, Osaka, Osaka 537, Japan
 (E-mail: suzuki@iph.pref.osaka.jp, Tel.: +81-6-972-1321,
 Fax: +81-6-972-0772)
 FEATURES Location/Qualifiers
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 DB 126 ACACACACAAATTCACAGAGCCCAAGAGGATGATGGTGAAGAGGATCCAGAGAA 185
 QY 181 GAGGGAAGCATGGCAAAAGTGGGACCGCATGGGCGCGAAGAAATTTAAAGGAGAACTGGGT 240
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 DB 666 ATGTTTACACAGACAAACACATCCACTGCGAGAACTATAGCAACTGGAATGAGGGGGAACCCAGC 725
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 DB 726 GACCCCTATGTTGTCATGAGAGTCTGTGAGATGCTGAGCTCTGCGAGATGGAATGACACA 785
 QY 781 GAGTGCATCTTACCATGCTACTTCTGCTGCTGAGTTCATCAAGAGAAAG 831
 DB 786 GAGTGCATCTTACCATGCTACTTCTGCTGCTGAGTTCATCAAGAGAAAG 836
 RESULT 2
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 LOCUS E29008 1595 bp DNA linear PAT 18-JUN-2001
 DEFINITION Novel collectin.
 ACCESSION E29008
 VERSION E29008.1 GI:13018416
 KEYWORDS JP 1999206377-A/1.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1595)
 AUTHORS Nobutake, W.
 TITLE Novel collectin
 JOURNAL Patent: JP 1999206377-A 1 03-AUG-1999;
 FUSO YAKUIN KOGYO KK
 COMMENT OS Homo sapiens (human)
 PN JP 1999206377-A/1
 PD 03-AUG-1999
 PF 23-JAN-1998 JP 1998011281
 PR NOBUTAKA WAKAMIYA
 PI C12N15/09, C07K14/47, C07K14/78, C12P21/00, C12N15/00 CC
 PC Strandedness: Double;
 CC Topology: Linear;
 FH Key Location/Qualifiers
 FT CDS Location/Qualifiers
 source 1..1595
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
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 Best Local Similarity 100.0%; Pred. No. 0;
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 QY 1 ATGAATGGCTTTGATCGCTTCTCGAAGAACCAATTTATCTCTGCTGCTACTATTTCTT 60
 DB 6 ATGAATGGCTTTGATCGCTTCTCGAAGAACCAATTTATCTCTGCTGCTACTATTTCTT 65
 QY 61 TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGCTCTACCGCTGAAGTCTGTGCC 120
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Db 246 GATATGGGAGATCGGGGCAATTTTGGCAAGACTGGGCCCAATTGGGAAGAGGGGTGACAAA 305
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QY 481 TACATCGTCAGGAGAGAGAACTACAGGGAATTCCTTACCCACTGCAGGATTCGGGT 540
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QY 781 GAGTGCCATCTTACCATGACTTTTGTCTGTGAGTTTCATCAAGAGAAAAAG 831
Db 786 GAGTGCCATCTTACCATGACTTTTGTCTGTGAGTTTCATCAAGAGAAAAAG 836

RESULT 3
AX376032 1016 bp DNA linear PAT 01-MAR-2002
LOCUS Sequence 99 from Patent WO0168848.
DEFINITION AX376032
ACCESSION AX376032.1 GI:19170408
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Baker,K.P., Chen,J., Desnoyers,L., Goddard,A., Godowski,P.J., Gurney,A.L., Pan,J., Smith,V., Watanabe,C.K., Wood,W.I. and Zhang,Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same
JOURNAL Patent: WO 0168848-A 99 20-SEP-2001;
Genentech, Inc. (US)
FEATURES
source Location/Qualifiers
1..1016
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 81.6%; Score 678; DB 6; Length 1016;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 241 GATATGGGAGATCGGGGCAATTTTGGCAAGCTGGGCCCATTTGGGAAGAGAGGTGACAAA 300
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QY 661 ATGTTTCAGACAAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGAAACCCAGC 720
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QY 781 GAGTGCCATCTTACCATGACTTTTGTCTGTGAGTTTCATCAAGAGAAAAAG 831
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RESULT 4
AX359038 1016 bp mRNA linear PRI 03-OCT-2003
LOCUS Homo sapiens clone DN50980 COLEC10 (UNQ366) mRNA, complete cds.
DEFINITION AX359038
ACCESSION AX359038.1 GI:37183193
VERSION
KEYWORDS FLI CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1016)
AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J., Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B., Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hase,P.E., Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S., Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C., Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V., Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K.,


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/rpt_family="MLTIC"
19051..19128
/rpt_family="AT-rich"
complement(19153..19244)

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Best Local Similarity 100.0%; Pred. No. 4.4e-207;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 442 GTGATAGCAGGATTAGGAACTGAAGAGAAATTTACTACATCGTGCAGGAGAGAAG 501
Db 55935 GTGATAGCAGGATTAGGAACTGAAGAGAAATTTACTACATCGTGCAGGAGAGAAG 55994

QY 502 AACTACAGGAAATCCCTAACCCACTGCAGGATTCGGGTGGAATGCTAGCATGCCCAAG 561
Db 55995 AACTACAGGAAATCCCTAACCCACTGCAGGATTCGGGTGGAATGCTAGCATGCCCAAG 56054

QY 562 GATGAGCTGCCAACACACTCATCGCTCACTATGTTGCCAGAGTGCCTTTTCGGGTG 621
Db 56055 GATGAGCTGCCAACACACTCATCGCTCACTATGTTGCCAGAGTGCCTTTTCGGGTG 56114

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Db 56175 CTGCAGAACTATAGCAACTGGAATGAGGGGAAACCCAGCGACCCCTATGTCATGAGGAC 56234

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Db 56235 TGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACAGAGTGCCTATCTTACCATGTAC 56294

QY 802 TTGTCTGTGAGTTCATCAAGAGAAAAG 831
Db 56295 TTGTCTGTGAGTTCATCAAGAGAAAAG 56324

RESULT 6
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LOCUS Homo sapiens chromosome 8 clone RP11-164H21, WORKING DRAFT
DEFINITION SEQUENCE, 3 unordered pieces.
ACCESSION AC023487
VERSION AC023487.10 GI:13357236
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP; HTGS_ACTIVEPIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 182475)
Abola,A.P., Bruno,D., Conn,L., Dela Rosa,M., Faulkner,D.,
Fedorov,S., Glukhov,S., Hansen,N., Herman,Z.S., Hyman,R.,
Mao,J., Komp,C., Kottler,S., Lam,B., Marathe,R., Miranda,M.,
Morehouse,A.J., Nguyen,M., Oefner,P., Palm,C.J., Ramirez,D.,
Southwick,A.M., Webb,C., Wilhelmy,J., Yu,S. and Davis,R.W.
Unpublished
2 (bases 1 to 182475)
Bruno,D., Conn,L., Dela Rosa,M., Faulkner,D., Federspiel,N.,
Glukhov,S., Hansen,N., Hyman,R., Mao,J., Marathe,R.,
Morehouse,A.J., Oefner,P., Palm,C.J., Ramirez,D., Wilhelmy,J.,
Yu,S. and Davis,R.W.
Direct Submission
Submitted (14-FEB-2000) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
USA
On Mar 16, 2001 this sequence version replaced gi:13324778.
----- Genome Center
Center: Stanford DNA Sequencing and Technology Development
Center
Center code: SDSTDC
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Web site: http://sequence-www.stanford.edu/group/human/
Contact: hum-info@sequence.stanford.edu
----- Project Information
Center Project name: 844
Center Clone name: RP11-164H21
----- Summary Statistics
Sequencing Vector: M13mp18; X02513; 98% of reads
Sequencing Vector: plasmid; plasmid_accession; 2% of reads
Chemistry: Dye-primer; 0% of reads
Chemistry: Dye-terminator Big Dye; 99% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 180260 bases at least Q40
Consensus quality: 180441 bases at least Q30
Consensus quality: 180507 bases at least Q20
Insert size: 178514; agarose-fp
Insert size: 182275; sum-of-contigs
Quality coverage: 8.1x in Q20 bases; agarose-fp
Quality coverage: 7.9x in Q20 bases; sum-of-contigs.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 42072: contig of 42072 bp in length
* 42073 42172: gap of unknown length
* 42173 109254: contig of 67082 bp in length
* 109255 109355: gap of unknown length
* 109355 182475: contig of 73121 bp in length.
FEATURES
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/clone="RP11-164H21"
/clone_lib="RPCI human BAC library 11"
1..42072
/note="assembly_name:Contig9
clone_end:7"
misc_feature 42173..109254
/note="assembly_name:Contig10"
misc_feature 109355..182475
/note="assembly_name:Contig11
clone_end:SP6"
ORIGIN
Query Match 46.9%; Score 390; DB 2; Length 182475;
Best Local Similarity 100.0%; Pred. No. 4.2e-207;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 442 GTGATAGCAGGATTAGGAACTGAAGAGAAATTTACTACATCGTGCAGGAGAGAAG 501
Db 6233 GTGATAGCAGGATTAGGAACTGAAGAGAAATTTACTACATCGTGCAGGAGAGAAG 6174
QY 502 AACTACAGGAAATCCCTAACCCACTGCAGGATTCGGGTGGAATGCTAGCATGCCCAAG 561
Db 6173 AACTACAGGAAATCCCTAACCCACTGCAGGATTCGGGTGGAATGCTAGCATGCCCAAG 6114
QY 562 GATGAGCTGCCAACACACTCATCGCTCACTATGTTGCCAGAGTGCCTTTTCGGGTG 621
Db 6113 GATGAGCTGCCAACACACTCATCGCTCACTATGTTGCCAGAGTGCCTTTTCGGGTG 6054
QY 622 TTCTTTGGCGTGAATGACCTTGAAAGGAGGAGACAGTACATGTTTCACAGACAACACTCCA 681
Db 6053 TTCTTTGGCGTGAATGACCTTGAAAGGAGGAGACAGTACATGTTTCACAGACAACACTCCA 5994
QY 682 CTGCAGAACTATAGCAACTGGAATGAGGGGAAACCCAGCGACCCCTATGTCATGAGGAC 741
Db 5993 CTGCAGAACTATAGCAACTGGAATGAGGGGAAACCCAGCGACCCCTATGTCATGAGGAC 5934
```


repeat_region complement(6525..6618)
repeat_region /rpt_family="MIR3"
7916..8154
repeat_region /rpt_family="L2"
8667..9349
repeat_region /rpt_family="MER20B"
9864..10032
repeat_region /rpt_family="(CAAA)n"
complement(10702..10796)
repeat_region /rpt_family="MIR"
10889..11017
repeat_region /rpt_family="L2"
11306..11335
repeat_region /rpt_family="AT_rich"
11463..11863
repeat_region /rpt_family="LIME3A"
12429..12459
repeat_region /rpt_family="AT_rich"
12744..12790
repeat_region /rpt_family="(TC)n"
14902..14964
repeat_region /rpt_family="MIR"
15022..15242
repeat_region /rpt_family="MIR"
15285..15339
repeat_region /rpt_family="L2"
complement(17157..17522)
repeat_region /rpt_family="MT1A1"
complement(18369..18896)
repeat_region /rpt_family="L2"
20547..20787
repeat_region /rpt_family="MIR"
21748..22031
repeat_region /rpt_family="AluSc"
complement(22326..22498)
repeat_region /rpt_family="MIR"
complement(23660..24110)
repeat_region /rpt_family="LIM10"
complement(24128..24173)
repeat_region /rpt_family="L2"
complement(24468..24544)
repeat_region /rpt_family="MIR"
24761..24928
repeat_region /rpt_family="MER104"
24929..25043
repeat_region /rpt_family="L2"
complement(25078..25375)
repeat_region /rpt_family="L2"
25566..25735
repeat_region /rpt_family="MIR3"
complement(26214..26289)
repeat_region /rpt_family="L2"
complement(26299..26358)
repeat_region /rpt_family="MLT1L"
complement(26439..26599)
repeat_region /rpt_family="MLT1L"
26973..27034
repeat_region /rpt_family="L2"
28388..28482
repeat_region /rpt_family="MERSA"
28512..28551
repeat_region /rpt_family="(GAAAA)n"
28633..28858
repeat_region /rpt_family="MIR"
29787..29859
repeat_region

Query Match 17.9%; Score 149; DB 9; Length 147414;
Best local Similarity 100.0%; Pred. No. 7.2e-72;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAATGGCTTCATCCTTCCTTCGATGATTTGATAGCGTCTACCGTGAAGTCTGTGCC 60
DB 128505 ATGAATGGCTTCATCCTTCCTTCGATGATTTGATAGCGTCTACCGTGAAGTCTGTGCC 128564

QY 61 TTGCAAAATTCAGAGTCTGGGTCTGGATATTTGATAGCGTCTACCGTGAAGTCTGTGCC 120
DB 128565 TTGCAAAATTCAGAGTCTGGGTCTGGATATTTGATAGCGTCTACCGTGAAGTCTGTGCC 128624
QY 121 ACACACACAAATTTCCACGAGGACCCCAAGG 149
DB 128625 ACACACACAAATTTCCACGAGGACCCCAAGG 128653

RESULT 8
AC023487 182475 bp DNA linear HTG 26-MAR-2001
LOCUS
DEFINITION Homo sapiens chromosome 8 clone RP11-164H21, WORKING DRAFT
SEQUENCE, 3 unordered pieces.
AC023487
AC023487.10 GI:13357236
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP; HTGS_ACTIVEFIN.
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 182475)
AUTHORS Abola.A.P., Bruno.D., Conn.L., Dela Rosa.M., Faulkner.D.,
Federspiel.N., Glukhov.S., Hansen.N., Herman.Z.S., Hyman.R.,
Mac.J., Komp.C., Kottler.S., Lam.B., Marathe.R., Miranda.M.,
Morehouse.A.J., Nguyen.M., Oefner.P., Palm.C.J., Ramirez.D.,
Southwick.A.M., Webb.C., Wilhelm.J., Yu.S. and Davis.R.W.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 182475)
AUTHORS Bruno.D., Conn.L., Dela Rosa.M., Faulkner.D., Federspiel.N.,
Glukhov.S., Hansen.N., Hyman.R., Mac.J., Marathe.R.,
Morehouse.A.J., Oefner.P., Palm.C.J., Ramirez.D., Wilhelm.J.,
Yu.S. and Davis.R.W.
TITLE Direct Submission
JOURNAL
SUBMITTED (14-FEB-2000) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
USA
COMMENT On Mar 16, 2001 this sequence version replaced gi:13324778.

----- Genome Center
Center: Stanford DNA Sequencing and Technology Development
Center
Center code: SDSTDC
Web site: http://sequence-www.stanford.edu/group/human/
Contact: hum-info@sequence.stanford.edu
----- Project Information
Center project name: 844
Center clone name: RP11-164H21
----- Summary Statistics

Sequencing Vector: M13mp18; X02513; 98% of reads
Chemistry: Dye-terminator; 0% of reads
Chemistry: Dye-terminator Big Dye; 98% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 180260 bases at least Q40
Consensus quality: 180441 bases at least Q30
Consensus quality: 180507 bases at least Q20
Insert size: 178614; agarose-fp
Insert size: 182275; sum-of-contigs
Quality coverage: 8.1x in Q20 bases; agarose-fp
Quality coverage: 7.9x in Q20 bases; sum-of-contigs.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 42072: contig of 42072 bp in length
* 42073 42172: gap of unknown length
* 42173 109254: contig of 67082 bp in length
* 109255 109354: gap of unknown length

* 109355 182475: contig of 73121 bp in length.

FEATURES

source
Location/Qualifiers
1..182475
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="8"
/clone="RP11-164H21"
/clone_lib="RPC1 human BAC library 11"
1..42072
/note="assembly_name:Contig9
clone_end:77"
misc_feature
42173..109254
/note="assembly_name:Contig10"
misc_feature
109355..182475
/note="assembly_name:Contig11
clone_end:SP6"

ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 7e-72; Length 182475;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAATGCTTTGGCATCTCTGCTTTCGAGAAACCAATTTATCTCTCTGGPACTATTCTT 60
Db 105635 ATGAATGCTTTGGCATCTCTGCTTTCGAGAAACCAATTTATCTCTCTGGPACTATTCTT 105694
QY 61 TTGCAATTCAGATCTGGTCTGGATTTGATAGCGTCTCCGCTGACGCTGAGTCTGTGCC 120
Db 105695 TTGCAATTCAGATCTGGTCTGGATTTGATAGCGTCTCCGCTGAGTCTGTGCC 105754
QY 121 ACACACACAAATTCACAGGACCCAAAGG 149
Db 105755 ACACACACAAATTCACAGGACCCAAAGG 105783

RESULT 9

HSU92547/c
LOCUS
DEFINITION Homo sapiens chromosome 8 STS, sequence tagged site.
ACCESSION U92547
VERSION U92547.1 GI:2564795
KEYWORDS STS.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Eutheria; Chordata; Vertebrata; Euteleostomi;
Mammalia; Catarrhini; Homnidae; Homo.
AUTHORS Pierce, J., Leach, R. and Naylor, S.
TITLE New STS markers for human chromosome 8
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 767)
AUTHORS Pierce, J., Leach, R. and Naylor, S.
TITLE Direct Submission
JOURNAL Submitted (10-MAR-1997) Pathology, UTHSCSA, 7703 Floyd Curl Drive, San Antonio, TX 78284, USA
FEATURES
source
Location/Qualifiers
1..767
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="8"
/map="8 pter-qter"
/cell_type="hamster (CHO)/human lymphocyte UV20H21-17
hybrid"
/clone_lib="LL08NS02 from Lawrence Livermore Laboratory"
/note="chromosome 8 flow sorted DNA"

ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 2.7e-23; Length 767;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 345 AGGTACTGTCTGTGATTTGCGAAGATACCGGAATTTGTTGGCAACTGGATATTAGTAT 404
Db 540 AGGTACTGTCTGTGATTTGCGAAGATACCGGAATTTGTTGGCAACTGGATATTAGTAT 481
QY 405 TGC 407
Db 480 TGC 478

RESULT 10

AC097055
LOCUS
DEFINITION Rattus norvegicus clone CH230-2F22, WORKING DRAFT SEQUENCE, 3
unordered pieces.
ACCESSION AC097055
VERSION GI:25007102
KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE

AUTHORS
1 (bases 1 to 234922)
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, P.R., Allen, C., Albrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbara, J., Benton, J., Bimaga, K., Blankenburg, K., Bonin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Honsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louseged, H., Lozados, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Mettzer, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Ogih, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savary, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Umami, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wlaczek, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G., and Gibbs, R.

TITLE

Unpublished
JOURNAL
REFERENCE
2 (bases 1 to 234922)
Worley, K.C.

TITLE

JOURNAL

AUTHORS

REFERENCE

AUTHORS

Submitted (06-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 234922)
Worley, K.C.

TITLE Direct Submission
JOURNAL Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

COMMENT On Nov 15, 2002 this sequence version replaced gi:23664540. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: T0US
 Center clone name: CH230-2F22
 ----- Summary Statistics
 Assembly program: Phrap; version 0.990329
 Consensus quality: 231210 bases at least Q40
 Consensus quality: 232236 bases at least Q30
 Consensus quality: 233086 bases at least Q20
 Estimated insert size: 241867; sum-of-contigs estimation
 Quality coverage: 11x in Q20 bases; sum-of-contigs estimation

 * NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 3 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 188689: contig of 188689 bp in length
 * 188690 188789: gap of unknown length
 * 188790 232956: contig of 44167 bp in length
 * 232957 233056: gap of unknown length
 * 233057 234922: contig of 1866 bp in length.

FEATURES Location/Qualifiers
 source
 1..234922
 /organism="Rattus norvegicus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10116"
 /clone="CH230-2F22"

ORIGIN
 Query Match 4.2%; Score 35; DB 2; Length 234922;
 Best Local Similarity 100.0%; Pred. No. 6.2e-08; Mismatches 0; Indels 0; Gaps 0;
 Matches 35; Conservative 0; Indels 0; Gaps 0;

QY 733 CATGAGGACTGTGGAGACTGTGAGCTGTGCTGGCAG 767
 |||||
 DB 14594 CATGAGGACTGTGGAGACTGTGAGCTGTGCTGGCAG 14628
 |||||

RESULT 11
 AB016429 867 bp mRNA linear ROD 07-JAN-2003
DEFINITION Mus musculus mRNA for collectin-L1, complete cds.
ACCESSION AB016429
VERSION AB016429.1 GI:27530340
KEYWORDS collectin-L1.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
 Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 1
AUTHORS Kawai, T., Suzuki, Y., Eda, S., Kase, T., Ohtani, K., Sakai, Y.,
 Keshi, H., Fukuchi, A., Sakamoto, T., Nozaki, M., Copeland, N.G.,
 Jenkins, N.A. and Wakamiya, N.
TITLE Molecular cloning of mouse collectin liver 1
JOURNAL Biotechmol. Biochem. 66 (10), 2134-2145 (2002)
MEDLINE 2333927
PUBMED 12450124
REFERENCE 2 (bases 1 to 867)
AUTHORS Kawai, T. and Suzuki, Y.
TITLE Direct Submission
JOURNAL Submitted (21-JUL-1998) Takao Kawai, Osaka Prefectural Institute of
 Public Health, Laboratory of Food Microbiology; 3-69 Nakamichi
 1-chome, Higashinari-ku, Osaka 537-0025, Japan
 (E-mail: kawai@iph.pref.osaka.jp; Tel:81-6-972-1321,
 Fax:81-6-972-2393)

FEATURES Location/Qualifiers
 source
 1..867
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL 6J"
 /db_xref="taxon:10090"
 /clone="mC11-N1C1-9"
 /tissue_type="liver"
 9..842
 /codon_start=1
 /product="collectin-L1"
 /protein_id="BAC53954.1"
 /db_xref="GI:27530341"
 /translation="MNGFVLLRSLMLLLALLHFLSGLDVSRAAEVCATHTI
 SPQKGDGERTDGEEDGKGVKQPGKVGELGDMGQNIKSGPFGKGGKGE
 KGLLHPGKRGAGTICDCGRYKVVQGLDISVRLKTSMKFIKNVIAGIRETEKFFY
 YIVCEKNYRESLTHCRIRGGLAMPKDSVNTLIADYVAKSGFRRFVIGVNDLEREG
 QYVETDTPLOYSNWKKEPSPSGHEDPCVEMLSGGRWDTCHLTWYFVCFVKKK
 K"

CDS
 458 GGGAACTGAAGAGAAATCTACTACAT 485
 |||||
 466 GGGAACTGAAGAGAAATCTACTACAT 493
 |||||

ORIGIN
 Query Match 3.4%; Score 28; DB 10; Length 867;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 458 GGGAACTGAAGAGAAATCTACTACAT 485
 |||||
 DB 466 GGGAACTGAAGAGAAATCTACTACAT 493
 |||||

RESULT 12
 AC115924 166900 bp DNA linear HTG 18-JUN-2003
LOCUS Mus musculus clone RP24-511011, WORKING DRAFT SEQUENCE, 4 ordered
DEFINITION pieces.
ACCESSION AC115924
VERSION AC115924.4 GI:31880195
KEYWORDS HTG; HTGS PHASE2; HTGS DRAFT; HTGS_FULLTOP.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 166900)
REFERENCE Birren, B., Nusbaum, C. and Lander, E.
AUTHORS Birren, B., Nusbaum, C. and Lander, E.
TITLE Mus musculus, clone RP24-511011
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 166900)
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
 Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L.,
 Bouckgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J.,
 Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collamore, A.,
 Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J. S., Dodge, S.,
 Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S.,
 Ginde, S., Gord, S., Goyette, N., Graham, L., Grand-Pierre, N.,

Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Lacroque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
Submitted (22-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 166900)

REFERENCE
AUTHORS
Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Bouckgatter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
Submitted (18-JUN-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 18, 2003 this sequence version replaced G121490462.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RN/RepeatMasker.html>

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L24895
Center clone name: 511_O_11
----- Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 165673 bases at least Q40
Consensus quality: 166156 bases at least Q30
Consensus quality: 166365 bases at least Q20
Insert size: 157000; agarose-ep
Quality coverage: 166600; sum-of-contigs
Quality coverage: 13.2 in Q20 bases; agarose-ep
Quality coverage: 12.4 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.

* This sequence will be replaced

* by the finished sequence as soon as it is available and
* the accession number will be preserved.

1 48320: contig of 48320 bp in length
48321 48420: gap of 100 bp
48421 59799: contig of 11379 bp in length
59800 59899: gap of 100 bp
59900 135830: contig of 75931 bp in length
135831 135931: gap of 100 bp
135932 166900: contig of 30970 bp in length.

FEATURES
Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="RP24-511011"
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/note="assembly_fragment
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vector_side:left"
48421..59799
/note="assembly_fragment"
59900..135830
/note="assembly_fragment"
135931..166900
/note="assembly_fragment
clone end:T7
vector_side:right"

ORIGIN
Query Match 3.4%; Score 28; DB 2; Length 166900;
Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 458 GCGAACTGAGAGAGAAATCTACTACAT 485
15164 GCGAACTGAGAGAGAAATCTACTACAT 15191

Db

RESULT 13
AC123656 222510 bp DNA linear HTG 27-MAR-2003
LOCUS
DEFINITION
Mus musculus clone RP23-188M21, WORKING DRAFT SEQUENCE, 6 unordered pieces.
AC123656
VERSION
AC123656.6 GI:29294284
KEYWORDS
HTG; HTGS PHASE1; HTGS DRAFT.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 222510)
Birren, B., Nusbaum, C. and Lander, E.
Mus musculus, clone RP23-188M21
Unpublished
JOURNAL
2 (bases 1 to 222510)
REFERENCE
AUTHORS
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Bouckgatter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazar, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Lacroque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Schuback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Straus, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
 Direct Submission
 Submitted (01-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 222510)
 Birren, B., Nusbaum, C., Lander, E., Abouelheil, A., Allen, N., Anderson, S., Arachchi, H. M., Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L., Boukhalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cooke, A., Cooke, P., Corum, B., DeArrellano, K., Diaz, J. S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Fero, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., O'Neil, R., O'Norris, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramaeamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V. S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
 Direct Submission
 Submitted (27-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Mar 27, 2003 this sequence version replaced gi:28626869.
 All repeats were identified using RepeatMasker.
 Smit, A. P. A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www.seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L26354
 Center clone name: 188 M 21
 ----- Summary Statistics
 Sequencing vector: plasmid; n/a; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.950731
 Consensus quality: 221635 bases at least Q40
 Consensus quality: 221908 bases at least Q30
 Consensus quality: 221986 bases at least Q20
 Insert size: 200000; agarose-tp
 Quality coverage: 10.7 in Q20 bases; sum-of-contigs
 Quality coverage: 9.6 in Q20 bases; sum-of-contigs

 * NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will be preserved. *
 1 2031: contig of 2031 bp in length
 2032
 2132: gap of 100 bp
 2132
 15244: contig of 13113 bp in length
 15245
 15344: gap of 100 bp
 15345
 37649: contig of 22305 bp in length
 37650
 37650: gap of 100 bp
 37750
 148108: contig of 110353 bp in length
 148103
 148203: gap of 100 bp
 148203
 190361: contig of 42159 bp in length

* 190362 190461: gap of 100 bp
 * 190462 222510: contig of 32049 bp in length.
 FEATURES
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 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 /clone_RP23-188M21"
 /clone_lib="RPC1-23 Female Mouse BAC"
 1..2031
 /note="assembly_fragment"
 2132..15244
 /note="assembly_fragment"
 15345..37649
 /note="assembly_fragment"
 37750..148102
 /note="assembly_fragment"
 148203..190361
 /note="assembly_fragment"
 190462..222510
 /note="assembly_fragment"
 clone_end:T7
 vector_side:right
 ORIGIN
 Query Match 3.4% Score 28; DB 2; Length 222510;
 Best Local Similarity 100.0%; Pred. No. 0.00053;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 458 GGGAACTGAGAGAAATTCCTACTACAT 485
 Db 157216 GGGAACTGAGAGAAATTCCTACTACAT 157243
 RESULT 14
 AC131337
 LOCUS
 DEFINITION Mus musculus clone RP23-480E1, WORKING DRAFT SEQUENCE, 17 unordered pieces.
 AC131337
 VERSION AC131337.4 GI:30017797
 KEYWORDS HTG; HTGS; PHASE1; HTGS_DRAFT.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Birren, B., Nusbaum, C. and Lander, E.
 Mus musculus, clone RP23-480E1
 Unpublished
 1 (bases 1 to 345420)
 2 (bases 1 to 345420)
 Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L., Boukhalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cooke, A., Cooke, P., DeArrellano, K., Dewar, K., Diaz, J. S., Dodge, S., Fero, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
 Direct Submission
 Submitted (20-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 345420)
 TITLE
 JOURNAL
 REFERENCE

AUTHORS

Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Bouchgallier, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., Dearellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, M., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kelle, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., Maclean, C., MacDonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Mesureux, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupbach, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
Submitted (23-APR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Apr 17, 2003 this sequence version replaced gi:28626850.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

TITLE
JOURNAL

COMMENT

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WISR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: 126504

Center clone name: 480_E_1

* NOTE: This is a 'working draft' sequence. It currently
* consists of 17 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
* be preserved.

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1 1221: contig of 1221 bp in length
* 1222 1321: gap of 100 bp
* 1322 2740: contig of 1419 bp in length
* 2741 2840: gap of 100 bp
* 2841 4351: contig of 1511 bp in length
* 4352 4451: gap of 100 bp
* 4452 7231: contig of 2780 bp in length
* 7232 7331: gap of 100 bp
* 7332 13580: contig of 6249 bp in length
* 13581 13680: gap of 100 bp
* 13681 19224: contig of 5544 bp in length
* 19225 19324: gap of 100 bp
* 19325 24245: contig of 4921 bp in length
* 24246 24345: gap of 100 bp
* 24346 33304: contig of 8959 bp in length
* 33305 33404: gap of 100 bp
* 33405 43959: contig of 10555 bp in length
* 43960 44059: gap of 100 bp
* 44060 64192: contig of 20133 bp in length
* 64193 64292: gap of 100 bp
* 64293 140233: contig of 75941 bp in length
* 140234 140333: gap of 100 bp
* 140334 166937: contig of 26604 bp in length
* 166938 167037: gap of 100 bp
* 167038 202564: contig of 35527 bp in length
* 202565 202664: gap of 100 bp
* 202665 235865: contig of 33201 bp in length
* 235866 235965: gap of 100 bp
* 235966 282239: contig of 46274 bp in length

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* 282240 282339: gap of 100 bp
* 282340 325240: contig of 42901 bp in length
* 325241 325340: gap of 100 bp
* 325341 345420: contig of 20080 bp in length.
FEATURES
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                /note="assembly_fragment"
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                /note="assembly_fragment"
            clone end:T7
            vector_side:right"
ORIGIN

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Query Match 3.4%; Score 28; DB 2; Length 345420;
Best Local Similarity 100.0%; Pred. No. 0.00049;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 458 GGGAACTGAAGAGAAATCTACTACAT 485
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Db 176241 GGGAACTGAAGAGAAATCTACTACAT 176268

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RESULT 15
AC117155/c

LOCUS AC117155 231676 bp DNA linear HTG 15-NOV-2002
DEFINITION Rattus norvegicus clone CH230-174N22, WORKING DRAFT SEQUENCE, 3
unordered pieces.

ACCESSION AC117155
VERSION AC117155.4 GI:25013203
KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 231676)
AUTHORS Muzny, D. Marie., Metzker, M. Lee., Abramson, S., Adams, C., Alder, J.,

Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Ayodeji, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bardarane, D., Barber, M., Barnstead, M., Benahmed, F., Blawie, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Esguerra-Rocha, S., Dunn, A., Durbin, K., Duval, B., Evans, K., Egan, A., Escoto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregorgis, E., Geet, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hayes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogue, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpach, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorenstehwa, L., Loulsegad, H., Lozado, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapa, P., Martin, K., Martin, R., Martinez, E., Mawhiney, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwankwelu, O., Okwuonu, G., Olarnpungoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfamkoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Puzo, M., Quintero, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, P., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, N., Savary, G., Scherer, S., Scott, G., Shatman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sison, I., Sitter, C.D., Smajic, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Taber, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wlezyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.

Direct Submission
Unpublished
2 (bases 1 to 231676)
Worley, K.C.

Direct Submission
Submitted (08-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 231676)
Rat Genome Sequencing Consortium.

Direct Submission
Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 15, 2002 this sequence version replaced gi:23194714.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome

shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GUGP
Center clone name: CH230-174N22

----- Summary Statistics

Assembly program: Phrap; version 0.990329
Consensus quality: 220570 bases at least Q40
Consensus quality: 222683 bases at least Q30
Consensus quality: 223867 bases at least Q20
Estimated insert size: 225142; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 229141: contig of 229141 bp in length
229142 229241: gap of unknown length
229242 230303: contig of 1062 bp in length
230304 230403: gap of unknown length
230404 231676: contig of 1273 bp in length.

FEATURES

source

1..231676
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clones="CH230-174N22"

misc_feature

1..1324

/note="wgs end extension"

clone_end:Sp6"

6422..6947

/note="clone boundary"

clone_end:Sp6

site:

end_sequence:BH350085"

complement(228397..228871)

/note="clone boundary"

clone_end:T7

site:

end_sequence:BH350083"

ORIGIN

Query Match 3.1%; Score 26; DB 2; Length 231676;
Best Local Similarity 100.0%; Pred. No. 0.0069;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 805 GTCGTGAGTTCATCAGACAGAAAA 830
Db 197764 GTCGTGAGTTCATCAGACAGAAAA 197739

Search completed: March 11, 2004, 20:30:18
Job time : 3304 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 16:59:01 ; Search time 396 Seconds
(without alignments)
8914.779 Million cell updates/sec

Title: US-09-600-932-1_COPY_6_836
Perfect score: 831
Sequence: 1 atgaatgcttgcattcctt.....agttcatcaagaagaaag 831

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_29Jan04.*

- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002s.*
- 7: Geneseqn2003as.*
- 8: Geneseqn2003bs.*
- 9: Geneseqn2003cs.*
- 10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	831	100.0	1595	2	AX88323 Human col
2	678	81.6	1016	2	Aaz33973 Human PRO
3	678	81.6	1016	3	AAC78480 Human PRO
4	678	81.6	1016	4	AAS45974 Human DNA
5	678	81.6	1016	7	ABX78577 Human PRO
6	678	81.6	1016	7	ACA75549 Novel hum
7	678	81.6	1016	7	ACA71029 Human sec
8	678	81.6	1016	7	ACC87557 Human sec
9	678	81.6	1016	7	ACC86943 Human sec
10	678	81.6	1016	7	ACD04116 Human sec
11	678	81.6	1016	7	ACA69447 cDNA enco
12	678	81.6	1016	7	ACA90292 Novel hum
13	678	81.6	1016	7	ACC83199 Human sec
14	678	81.6	1016	7	ACA98190 Novel hum
15	678	81.6	1016	7	ACA93832 Human sec
16	678	81.6	1016	7	ACD15225 Human sec
17	678	81.6	1016	7	ACD08812 Human sec
18	678	81.6	1016	7	ACC96732 Human sec
19	678	81.6	1016	7	ACF15453 Human sec
20	678	81.6	1016	7	ACD42506 Novel hum
21	678	81.6	1016	7	ACA72820 Human PRO
22	678	81.6	1016	7	ACD02992 Novel hum
23	678	81.6	1016	7	ACD01807 Novel hum

24	678	81.6	1016	7	ACA91999 Novel hum
25	678	81.6	1016	7	ACA63541 Novel hum
26	678	81.6	1016	7	ACA89424 cDNA enco
27	678	81.6	1016	7	ACA73434 Human sec
28	678	81.6	1016	7	ACA05749 Human sec
29	678	81.6	1016	7	ACA65583 cDNA enco
30	678	81.6	1016	7	ACF20158 Human sec
31	678	81.6	1016	7	ACF19544 Human sec
32	678	81.6	1016	7	ACD21832 Human sec
33	678	81.6	1016	7	ACF12997 Human sec
34	678	81.6	1016	7	ACD25100 Human sec
35	678	81.6	1016	7	ACF00149 Human sec
36	678	81.6	1016	7	ACA72206 Novel hum
37	678	81.6	1016	7	ACD04730 Novel hum
38	678	81.6	1016	7	ACD18191 Human sec
39	678	81.6	1016	7	ACD08198 Human sec
40	678	81.6	1016	7	ACA88632 Novel hum
41	678	81.6	1016	7	ACA70074 Human sec
42	678	81.6	1016	7	ACD12296 Novel hum
43	678	81.6	1016	7	ACC74211 Human sec
44	678	81.6	1016	7	ACD15839 Human sec
45	678	81.6	1016	7	ACD25407 Novel hum

ALIGNMENTS

RESULT 1
AX88323
ID AX88323 standard; cDNA; 1595 BP.
XX
AC AAX88323;
XX
DT 30-SEP-1999 (first entry)
XX
DE Human collectin cDNA.
XX
KW Collectin; human; antibacterial; antiviral; treatment; infection; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 6...839
FT /*tag= a
FT /product= "collectin"
XX
PN WO9937767-A1.
XX
PD 29-JUL-1999.
XX
PF 24-JUL-1998; 98WO-JP003328.
XX
PR 23-JAN-1998; 98JP-00011281.
XX
PA (FUSO) FUSO PHARM IND LTD.
XX
PI Wakamiya N;
XX
DR WPI; 1999-458691/38.
XX
P-PSDB; AAY25518.
XX
PT New collectin protein of human origin and DNA encoding it.
XX
PS Claim 2; Page 39-42; 58pp; Japanese.
XX
CC This invention describes the isolation and characterisation of a novel human collectin protein and its encoding polynucleotide. The human collectin exhibits antibacterial and antiviral activity and can be used as an agent for the treatment of human bacterial and viral infections.
XX
CC This sequence encodes the novel human collectin
SQ Sequence 1595 BP; 444 A; 322 C; 382 G; 447 T; 0 U; 0 Other;

Query Match 100.0%; Score 831; DB 2; Length 1595;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 831; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGATGGCTTGGCATCTTCTGCGAAGAACCAATTTATCTCTCTGCTACTATTTCTT	60
Db	6	ATGATGGCTTGGCATCTTCTGCGAAGAACCAATTTATCTCTCTGCTACTATTTCTT	65
Qy	61	TTGCAAAATTCAGAGTCTGGTCTGGATATGATAGCCCTCTACCGCTGAAGTCTGTGC	120
Db	66	TTGCAAAATTCAGAGTCTGGTCTGGATATGATAGCCCTCTACCGCTGAAGTCTGTGC	125
Qy	121	ACACACACAAATTCACAGGCCACCAAGAGATGATGTGAAAGAGATCCAGAGAA	180
Db	126	ACACACACAAATTCACAGGCCACCAAGAGATGATGTGAAAGAGATCCAGAGAA	185
Qy	181	GAGGGAAGCATGGCAAGTGGGAGCGATGGGGCGAAAGGAATTAAGGAGAACTGGGT	240
Db	186	GAGGGAAGCATGGCAAGTGGGAGCGATGGGGCGAAAGGAATTAAGGAGAACTGGGT	245
Qy	241	GATATGGGAGATCGGGGCAATTTGCGAAGACTGGGCCATTTGGGAAGAGGTGACAA	300
Db	246	GATATGGGAGATCGGGGCAATTTGCGAAGACTGGGCCATTTGGGAAGAGGTGACAA	305
Qy	301	GGGGAAAAAGTTTCTTGGATACCTGGGAAGAAAGCAAGCAGTACTGTCTGTGAT	360
Db	306	GGGGAAAAAGTTTCTTGGATACCTGGGAAGAAAGCAAGCAGTACTGTCTGTGAT	365
Qy	361	TGTGGAGATACCGGAATTTGTGGCAACTGAGATATAGTATGTCGGCTCAAGACA	420
Db	366	TGTGGAGATACCGGAATTTGTGGCAACTGAGATATAGTATGTCGGCTCAAGACA	425
Qy	421	TCTATGAAGTTTGTCAAGATGTGATAGCAGGGATTAGGGAACTGAAGAGAAATTTCTAC	480
Db	426	TCTATGAAGTTTGTCAAGATGTGATAGCAGGGATTAGGGAACTGAAGAGAAATTTCTAC	485
Qy	481	TACATCGTCGAGAGAGAGAACTACAGGGAATCCCTAACCCCTCGCAGGATTCGGGGT	540
Db	486	TACATCGTCGAGAGAGAGAACTACAGGGAATCCCTAACCCCTCGCAGGATTCGGGGT	545
Qy	541	GGATCTAGCATGCCCAAGATGAAGCTGCAACACACATCATCGCTGCTATGTTGCC	600
Db	546	GGATCTAGCATGCCCAAGATGAAGCTGCAACACACATCATCGCTGCTATGTTGCC	605
Qy	601	AGAGTGGCTTTCTTGGGTGTTCTTGGGTGATGATGACCTTGAAGAGGAGGACAGTAC	660
Db	606	AGAGTGGCTTTCTTGGGTGTTCTTGGGTGATGATGACCTTGAAGAGGAGGACAGTAC	665
Qy	661	ATGTTACAGACAACTCCACTGACAGACTATAGCACTGGAATGAGGGGACCCAGC	720
Db	666	ATGTTACAGACAACTCCACTGACAGACTATAGCACTGGAATGAGGGGACCCAGC	725
Qy	721	GACCCCTATGCTCATGAGACTGTGAGATGCTGAGCTTGCAGATGGAATGACACA	780
Db	726	GACCCCTATGCTCATGAGACTGTGAGATGCTGAGCTTGCAGATGGAATGACACA	785
Qy	781	GAGTGCCTTACCATTGCTGTTCTGTTGATGATCATCAAGAGAAAG	831
Db	786	GAGTGCCTTACCATTGCTGTTCTGTTGATGATCATCAAGAGAAAG	836

RESULT 2
AAZ33973
ID AAZ33973 standard; cDNA; 1016 BP.
XX AAZ33973;
AC AAZ33973;
DT 07-DEC-1999 (first entry)
XX Human PR0702 nucleotide sequence.
DX Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;

secreted protein; transmembrane protein; ss.

Homo sapiens.

WO9946281-A2.

16-SEP-1999.

08-MAR-1999; 99WO-US005028.

10-MAR-1998; 98US-0077450P.

11-MAR-1998; 98US-0077632P.

11-MAR-1998; 98US-0077641P.

11-MAR-1998; 98US-0077649P.

12-MAR-1998; 98US-0077791P.

13-MAR-1998; 98US-0078004P.

17-MAR-1998; 98US-00040220.

20-MAR-1998; 98US-0078886P.

20-MAR-1998; 98US-0078910P.

20-MAR-1998; 98US-0078936P.

20-MAR-1998; 98US-0078939P.

25-MAR-1998; 98US-0079294P.

26-MAR-1998; 98US-0079656P.

27-MAR-1998; 98US-0079663P.

27-MAR-1998; 98US-0079664P.

27-MAR-1998; 98US-0079728P.

27-MAR-1998; 98US-0079786P.

30-MAR-1998; 98US-0079920P.

30-MAR-1998; 98US-0079923P.

31-MAR-1998; 98US-0080105P.

31-MAR-1998; 98US-0080107P.

31-MAR-1998; 98US-0080165P.

31-MAR-1998; 98US-0080194P.

01-APR-1998; 98US-0080327P.

01-APR-1998; 98US-0080328P.

01-APR-1998; 98US-0080333P.

01-APR-1998; 98US-0080334P.

08-APR-1998; 98US-0081049P.

08-APR-1998; 98US-0081070P.

08-APR-1998; 98US-0081071P.

09-APR-1998; 98US-0081195P.

09-APR-1998; 98US-0081203P.

09-APR-1998; 98US-0081229P.

15-APR-1998; 98US-0081817P.

15-APR-1998; 98US-0081838P.

15-APR-1998; 98US-0081952P.

15-APR-1998; 98US-0081955P.

21-APR-1998; 98US-0082568P.

21-APR-1998; 98US-0082569P.

22-APR-1998; 98US-0082700P.

22-APR-1998; 98US-0082704P.

22-APR-1998; 98US-0082804P.

23-APR-1998; 98US-0082767P.

23-APR-1998; 98US-0082796P.

27-APR-1998; 98US-0083336P.

28-APR-1998; 98US-0083322P.

29-APR-1998; 98US-0083392P.

29-APR-1998; 98US-0083495P.

29-APR-1998; 98US-0083496P.

29-APR-1998; 98US-0083499P.

29-APR-1998; 98US-0083500P.

29-APR-1998; 98US-0083545P.

29-APR-1998; 98US-0083554P.

29-APR-1998; 98US-0083558P.

29-APR-1998; 98US-0083559P.

30-APR-1998; 98US-0083742P.

05-MAY-1998; 98US-0083666P.

06-MAY-1998; 98US-0084414P.

06-MAY-1998; 98US-0084441P.

07-MAY-1998; 98US-0084598P.

07-MAY-1998; 98US-0084600P.

07-MAY-1998; 98US-0084627P.

PR 07-MAY-1998; 98US-0084637P.
 PR 07-MAY-1998; 98US-0084639P.
 PR 07-MAY-1998; 98US-0084640P.
 PR 07-MAY-1998; 98US-0084643P.
 PR 13-MAY-1998; 98US-0085323P.
 PR 13-MAY-1998; 98US-0085328P.
 PR 13-MAY-1998; 98US-0085338P.
 PR 13-MAY-1998; 98US-0085339P.
 PR 15-MAY-1998; 98US-0085573P.
 PR 15-MAY-1998; 98US-0085579P.
 PR 15-MAY-1998; 98US-0085580P.
 PR 15-MAY-1998; 98US-0085582P.
 PR 15-MAY-1998; 98US-0085689P.
 PR 15-MAY-1998; 98US-0085697P.
 PR 15-MAY-1998; 98US-0085700P.
 PR 15-MAY-1998; 98US-0085704P.
 PR 18-MAY-1998; 98US-0086023P.
 PR 22-MAY-1998; 98US-0086392P.
 PR 22-MAY-1998; 98US-0086414P.
 PR 22-MAY-1998; 98US-0086430P.
 PR 22-MAY-1998; 98US-0086486P.
 PR 28-MAY-1998; 98US-0087098P.
 PR 28-MAY-1998; 98US-0087106P.
 PR 28-MAY-1998; 98US-0087208P.
 PR 30-JUL-1998; 98US-0094651P.
 PR 11-SEP-1998; 98US-0100038P.
 XX
 PA (GETH) GENENTECH INC.

Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;

WPI; 1999-551358/46.
 P-PSDB; AAY41698.

New secreted and transmembrane polypeptides and their polynucleotides,
 useful for treating blood coagulation disorders, cancers and cellular
 adhesion disorders.

Claim 2; Fig 36; 530pp; English.

The present invention describes secreted and transmembrane polypeptides
 and their polynucleotides. The nucleotide sequences are useful as sources
 of probes, primers, for chromosome mapping, and for generation of
 antisense sequences. They can also be used to create transgenic animals.
 The proteins can be used to treat a variety of diseases and disorders,
 depending on their function. Diseases that may be treated include blood
 coagulation disorders, cancers and cellular adhesion disorders. They may
 also be used to raise antibodies. AA233891 to AA234338, and AAY41685 to
 AAY41774 represent polynucleotide and polypeptide sequence given in the
 exemplification of the present invention

Sequence 1016 BP; 312 A; 197 C; 261 G; 246 T; 0 U; 0 Other;

Query Match 81.6%; Score 678; DB 2; Length 1016;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGAATGGCTTTCATCTGCTTGCAGAACACCAATTTATCTCTGGTACTATTTCTT 60
 DB 22 ATGAATGGCTTTCATCTGCTTGCAGAACACCAATTTATCTCTGGTACTATTTCTT 81
 QY 61 TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGCTCTACCGCTGAAGTCTGTGCC 120
 DB 82 TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGCTCTACCGCTGAAGTCTGTGCC 141
 QY 121 ACACACACATTTACACAGACCCAAAGAGATGATGTGAAAAGAGATCCAGGAGAA 180
 DB 142 ACACACACATTTACACAGACCCAAAGAGATGATGTGAAAAGAGATCCAGGAGAA 201
 QY 181 GAGCGAAAGCATGGCAAGTGGGAGCATGGGCGCCGAAGGAATTAAGAGAGAACTGGGT 240
 DB 202 GAGCGAAAGCATGGCAAGTGGGAGCATGGGCGCCGAAGGAATTAAGAGAGAACTGGGT 261
 QY 241 GATATGGGAGATCGGGGCGCAATTTGGCAAGACTGGGCCCATTTGGGAGAGAGGGTGACAAA 300

DB 262 GATATGGGAGATCAGGGCAATATTGGCAAGACTGGGCCCATTTGGAAAGAGGGTGACAAA 321
 QY 301 GGGGAAAAGAGGTTTCTTGGGAATCCTGGAGAAAAGCAAGAGGAGTACTGTCTGTGAT 360
 DB 322 GGGGAAAAGAGGTTTCTTGGGAATCCTGGAGAAAAGCAAGAGGAGTACTGTCTGTGAT 381
 QY 361 TGTGGAAGATACCGGAAATTTTGTGGCAAACTGGATATTAGTATGCCCGCTCAAGACA 420
 DB 382 TGTGGAAGATACCGGAAATTTTGTGGCAAACTGGATATTAGTATGCCCGCTCAAGACA 441
 QY 421 TCTATCAAGTTTGTCAAGATGTGATAGCAGGGATAGGGAATCTGAAGAAAATTTCTAC 480
 DB 442 TCTATCAAGTTTGTCAAGATGTGATAGCAGGGATAGGGAATCTGAAGAAAATTTCTAC 501
 QY 481 TACATCGTGCAGGAAGAGAACTACAGGGAATCCCTAACCCACTGCGAGATTTCGGGGT 540
 DB 502 TACATCGTGCAGGAAGAGAACTACAGGGAATCCCTAACCCACTGCGAGATTTCGGGGT 561
 QY 541 GGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACAACACTCATCGCTGACTATGTTGCC 600
 DB 562 GGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACAACACTCATCGCTGACTATGTTGCC 621
 QY 601 AAGAGTGGCTTCTTTTCGGGTGTTTCAATGGCTGATGACCTTGAAGAGGGGACAGTAC 660
 DB 622 AAGAGTGGCTTCTTTTCGGGTGTTTCAATGGCTGATGACCTTGAAGAGGGGACAGTAC 681
 QY 661 ATGTTTCACAGACACACTCCACTGCAGAACTATAGCACTGGAATGAGGGGACCCAGC 720
 DB 682 ATGTTTCACAGACACACTCCACTGCAGAACTATAGCACTGGAATGAGGGGACCCAGC 741
 QY 721 GACCCCTATGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGCGAGATGGAATGACACA 780
 DB 742 GACCCCTATGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGCGAGATGGAATGACACA 801
 QY 781 GAGTGGCATCTACCATGTACTTTGCTGTGAGTCTCATGAGAGGAAAG 831
 DB 802 GAGTGGCATCTACCATGTACTTTGCTGTGAGTCTCATGAGAGGAAAG 852

RESULT 3

AAC78480
 ID AAC78480 standard; cDNA; 1016 BP.
 XX AAC78480;
 DT 08-FEB-2001 (first entry)
 XX Human PRO702 (UNQ366) nucleotide sequence SEQ ID NO:96.
 XX Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;
 XX expressed sequence tag; detection; cancer; ss.
 OS Homo sapiens.
 XX WO2000053756-A2.
 XX 14-SEP-2000.
 PF 18-FEB-2000; 2000WO-US004341.
 XX 08-MAR-1999; 99WO-US005028.
 PR 12-MAR-1999; 99US-0123957P.
 PR 29-MAR-1999; 99US-0126773P.
 PR 21-APR-1999; 99US-0130232P.
 PR 28-APR-1999; 99US-0131445P.
 PR 14-MAY-1999; 99US-0134287P.
 PR 23-JUN-1999; 99US-0141037P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 29-OCT-1999; 99US-0162506P.
 PR 30-NOV-1999; 99WO-US028313.
 PR 02-DEC-1999; 99WO-US028851.
 PR 02-DEC-1999; 99WO-US0288565.

PR 16-DEC-1999; 99WO-US0300095.
PR 30-DEC-1999; 99WO-US0312143.
PR 30-DEC-1999; 99WO-US0312174.
PR 05-JAN-2000; 2000WO-US0002119.
PR 05-JAN-2000; 2000WO-US0002177.
PR 06-JAN-2000; 2000WO-US0003746.
XX
XX (GETH) GENENTECH INC.
PA

PI Ashkenazi AJ Baker KP, Botstein D, Deenoyers L, Eaton DL;
 PI Perrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
 PI Godowski P, Grimaldi CU, Gurney AL, Hillan KJ,
 PI Kladaván IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy WA, Shelton DL;
 PI Stewart TA, Tumas D, Williams BW, Wood WI;
 XX WPI; 2000-611443/58.
 DR P-PSDB; AAB44254.
 DR P-PSDB; AAB44254.

Novel PRO polypeptides and polynucleotides used in detection methods, to target bioactive molecules to specific cells, and to modulate cellular activities.

PS Claim 2; Fig 36; 636pp; English.

CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence
CC tag) sequences which encode secreted or transmembrane PRO polypeptides.
CC The PRO polynucleotides and polypeptides have cytosolic activity. The
CC polynucleotides and polypeptides can be used for detecting the presence
CC of PRO polypeptides in samples, for linking bioactive molecules to cells
CC and for modulating biological activities of cells, using the polypeptides
CC for specific targeting. The polypeptide targeting can be used to kill the
CC target cells, e.g. for the treatment of cancers. The polypeptide pairs
CC provide specific targeting of bioactive molecules to cells. AAC78600 to
CC AAC78987 represent PCR primers and probes used in the isolation of the
CC PRO polynucleotide sequences

Sequence 1016 BP; 312 A; 197 C; 261 G; 246 T; 0 U; 0 Other;

Query Match	81.6%	Score 678;	DB 3;	Length 1016;
Best Local Similarity	99.6%;	Pred. No. 0;		
Matches 828;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;

QY	1	ATGAATGCGCTTTGCATCCTTCTGCTTCGAAGAAACAAATTTATCTCCTCGTGTACTATTCTT	60
DB	22	ATGAATGCGCTTTGCATCCTTCTGCTTCGAAGAAACAAATTTATCTCCTCGTGTACTATTCTT	81
QY	61	TTGCAAAATTCAGAGTCTGGGCTCTGGATATTGATAGCGGCTCTACCGCTCAAGCTCTGTGTGCC	120
DB	82	TTGCAAAATTCAGAGTCTGGGCTCTGGATATTGATAGCGGCTCTACCGCTCAAGCTCTGTGTGCC	141

Qy	481	TACATCGTCGAGGAAGAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGGGT	540
Db	502	TACATCGTCGAGGAAGAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGGGT	561
Qy	541	GGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACACACTATCCTGACTATGTTGCC	600
Db	562	GGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACACACTATCCTGACTATGTTGCC	621
Qy	601	AGAGTGGCTCTTTTCGGGTGTTCAATGGCGTGAATGACCTTCAAGGGAGGGACAGTAC	660
Db	622	AGAGTGGCTCTTTTCGGGTGTTCAATGGCGTGAATGACCTTCAAGGGAGGGACAGTAC	681
Qy	661	ATGTGTCACAGACAACACTCCACTGCAGAACTATAGCAACTGGAAATCAGGGGGAACCCAGC	720
Db	682	ATGTGTCACAGACAACACTCCACTGCAGAACTATAGCAACTGGAAATCAGGGGGAACCCAGC	741
Qy	721	GACCCCTATGTCATGAGGACTGTGTGGACATGCTGAGCTCTCGCAGATGGAATGACACA	780
Db	742	GACCCCTATGTCATGAGGACTGTGTGGACATGCTGAGCTCTCGCAGATGGAATGACACA	801
Qy	781	GAGTGCCATCTTACCATGTACTTTGCTGTGAGTTCAACAAGAGAAAAAG	831
Db	802	GAGTGCCATCTTACCATGTACTTTGCTGTGAGTTCAACAAGAGAAAAAG	852

RESULT 4

AAS45974
ID AAS45974 standard; cDNA; 1016 BP.

AAS45974;

18-DEC-2001 (first entry)

DE Human DNA encoding PRO polypeptide sequence #50.

XX PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
KW PCR primer.

xx Homo sapiens.

XX PN WO200168848-A2

XX
PD
20-SEP-2001

28-FEB-2001: 2001WO-IIS006520.

XX	01-MAR-2000;	2000WO-US005601.
PR	02-MAR-2000;	2000WO-US005841.
PR	03-MAR-2000;	2000US-0187202P.
PR	06-MAR-2000;	2000US-0186969P.
PR	14-MAR-2000;	2000US-0189320P.
PR	15-MAR-2000;	2000US-0189328P.
PR	15-MAR-2000;	2000WO-US006884.
PR	21-MAR-2000;	2000US-0190828P.
PR	21-MAR-2000;	2000US-0191007P.
PR	21-MAR-2000;	2000US-0191048P.
PR	22-MAR-2000;	2000US-0191314P.
PR	28-MAR-2000;	2000US-0194655P.
PR	29-MAR-2000;	2000US-0193032P.
PR	29-MAR-2000;	2000US-0193053P.
PR	30-MAR-2000;	2000WO-US008439.
PR	04-APR-2000;	2000US-0194449P.
PR	04-APR-2000;	2000US-0194647P.
PR	11-APR-2000;	2000US-0195975P.
PR	11-APR-2000;	2000US-0196060P.
PR	11-APR-2000;	2000US-0196187P.
PR	11-APR-2000;	2000US-0196690P.
PR	11-APR-2000;	2000US-0196820P.
PR	18-APR-2000;	2000US-0198121P.

PR 18-APR-2000; 2000US-0198585P.
 PR 25-APR-2000; 2000US-0199397P.
 PR 25-APR-2000; 2000US-0199550P.
 PR 25-APR-2000; 2000US-0199654P.
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 PR 02-JUN-2000; 2000WO-US015264.
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 PR 20-DEC-2000; 2000WO-US034956.
 XX
 PA (GETH) GENENTECH INC.
 XX
 XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
 XX
 DR WPI; 2001-602746/68.
 DR P-PSDB; AAU29073.
 XX
 PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the
 PT presence of tumors, such as prostate and breast tumors, in mammals and to
 PT screen for modulators of the compounds.
 XX
 XX Claim 2; Fig 99; 774pp; English.
 PS
 XX Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR
 CC primers for PRO polypeptides of the invention. The sequences of the
 CC invention can be used to detect the presence of a tumor in a mammal by
 CC comparing the level of expression of a PRO polypeptide in a test sample
 CC of cells from the animal and a control sample of normal cells, whereby a
 CC higher level of expression in the test sample indicates the presence of a
 CC tumor in the mammal. Mammals include dogs, cats, cattle, horses, sheep,
 CC pigs, goats and rabbits but are preferably human. The polypeptides can be
 CC used to stimulate tumour necrosis factor (TNF) alpha release from human
 CC blood, when contacted with it. A specific polypeptide can be used to
 CC stimulate the proliferation or differentiation of chondrocyte cells. The
 CC PRO proteins can be used to determine the presence of tumours and also
 CC susceptibility to tumour development, particularly adrenal, lung, colon,
 CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
 CC can be used for genetic analysis of individuals with genetic disorders
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Qy	541	GGAAATGCTAGCCATGCCCAAGATGAAGTCCCAACACACTCATCTGCTGATGTGCC	600	PR	13-NOV-1997; 97US-0065311P.
Db	562	GGAAATGCTAGCCATGCCCAAGATGAAGTCCCAACACACTCATCTGCTGATGTGCC	621	PR	21-NOV-1997; 97US-0066120P.
Qy	601	AAGATGGCTTTCTTTCGGGTGTTTCATTCGGCTGATGACCTTGAAGGGAGGACAGTAC	660	PR	24-NOV-1997; 97US-0066466P.
Db	622	AAGATGGCTTTCTTTCGGGTGTTTCATTCGGCTGATGACCTTGAAGGGAGGACAGTAC	681	PR	11-DEC-1997; 97US-0069335P.
Qy	661	ATGTTCAAGACAACTCCACTGAGAACTATAGCACTGGAATAGGGGGGAAACCCAGC	720	PR	12-DEC-1997; 97US-0069425P.
Db	682	ATGTTCAAGACAACTCCACTGAGAACTATAGCACTGGAATAGGGGGGAAACCCAGC	741	PR	17-DEC-1997; 97US-0069870P.
Qy	721	GACCCCTATGTCATGAGACTGTGTGAGATGCTGAGCTCTGCGCATGGAATGACACA	780	PR	18-DEC-1997; 97US-0068017P.
Db	742	GACCCCTATGTCATGAGACTGTGTGAGATGCTGAGCTCTGCGCATGGAATGACACA	801	PR	10-MAR-1998; 98US-0077450P.
Qy	781	GAGTGCCATCTTACCATGCTACTTTGCTGCTGAGTTCATCAAGAGAAAAAG	831	PR	11-MAR-1998; 98US-0077632P.
Db	802	GAGTGCCATCTTACCATGCTACTTTGCTGCTGAGTTCATCAAGAGAAAAAG	852	PR	11-MAR-1998; 98US-0077632P.
RESULT 7					20-MAR-1998; 98US-0078886P.
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XX					31-MAR-1998; 98US-0080107P.
XX					31-MAR-1998; 98US-0080194P.
XX					01-APR-1998; 98US-0080327P.
DT	02-AUG-2003 (first entry)				01-APR-1998; 98US-0080333P.
DE	Human secreted/transmembrane protein (PRO) cDNA #50.				08-APR-1998; 98US-0081049P.
XX					08-APR-1998; 98US-0081070P.
KW	Human; gene; ss; secreted and transmembrane protein; PRO; TNF-alpha;				09-APR-1998; 98US-0081195P.
KW	tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;				15-APR-1998; 98US-0081838P.
KW	tissue typing.				21-APR-1998; 98US-0082568P.
XX					21-APR-1998; 98US-0082569P.
OS	Homo sapiens.				22-APR-1998; 98US-0082704P.
XX					22-APR-1998; 98US-0082797P.
PN	US2003032112-A1.				28-APR-1998; 98US-0083322P.
XX					29-APR-1998; 98US-0083495P.
					29-APR-1998; 98US-0083496P.
					29-APR-1998; 98US-0083499P.
					05-MAY-1998; 98US-0083559P.
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Query Match 81.6%; Score 678; DB 7; Length 1016;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 22 ATGAATGGCTTTGGCATCCTTGGCTTGAAGAAACCAATTTATCCTCTCTGTACTATTCTTT 81
QY 61 TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCGCTCCTACCGCTCAAGTCTGTGCC 120
DB 82 TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCGCTCCTACCGCTCAAGTCTGTGCC 141
QY 121 ACACACAAATTTCCAGAGCCCAAGAGAGATGTTGTAAGAGAGATCCAGAGAA 180
DB 142 ACACACAAATTTCCAGAGCCCAAGAGAGATGTTGTAAGAGAGATCCAGAGAA 201
QY 191 GAGGGAAGCATGCGCAAGTGGGACGCGATGGGCCGGAAGGAAATTAAGAGAGAACTGGGT 240
DB 202 GAGGGAAGCATGCGCAAGTGGGACGCGATGGGCCGGAAGGAAATTAAGAGAGAACTGGGT 261
QY 241 GATATGGGAGATCGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGAGGGGTGACAA 300
DB 262 GATATGGGAGATCAGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGAGGGGTGACAA 321
QY 301 GGGGAAAGGTTTGGTGGATACCTTGGGAAAGGCAAGCAGGTACTGTCTGTGAT 360
DB 322 GGGGAAAGGTTTGGTGGATACCTTGGGAAAGGCAAGCAGGTACTGTCTGTGAT 381
QY 361 TGTGAAGATACCGGAAATTTGTGGCAACTGATATTAGTATTCGCCGCTCAAGACA 420
DB 382 TGTGAAGATACCGGAAATTTGTGGCAACTGATATTAGTATTCGCCGCTCAAGACA 441
QY 421 TCTATGAAGTTTGTCAAGATGTTAGGAGGATTTAGGGAAGTCTGAGAAATTTCTAC 480

Db 442 TCTATGAAGTTGTCAAGAATGTGATAGCAGGGAATTAGGGAACCTGAAGAGAAATCTTAC 501
QY 481 TACATCGTGCAGGAGAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGGGGT 540
Db 502 TACATCGTGCAGGAGAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGGGGT 561
QY 541 GGAATGCTAGCATGCCCAAGGATGAAGCTGCCAACACACTCATCGCTGACTATGTTGCC 600
Db 562 GGAATGCTAGCATGCCCAAGGATGAAGCTGCCAACACACTCATCGCTGACTATGTTGCC 621
QY 601 AAGAGTGGCTTTCTCGGGTGTTCATTGGCGTGAATGACCTTGAAGGGAGGACAGTAC 660
Db 622 AAGAGTGGCTTTCTCGGGTGTTCATTGGCGTGAATGACCTTGAAGGGAGGACAGTAC 681
QY 661 ATGTTCCAGACACACTCCACTGCAGACTATAGCACTTGAATGAGGGGGGACCCAGC 720
Db 682 ATGTTCCAGACACACTCCACTGCAGACTATAGCACTTGAATGAGGGGGGACCCAGC 741
QY 721 GACCCCTATGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGCAGATGGAATGACACA 780
Db 742 GACCCCTATGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGCAGATGGAATGACACA 801
QY 781 GAGTCCCATCTTACATGACTATTTGTTCTGTGAGTTCTATCAAGAGAAAAG 831
Db 802 GAGTCCCATCTTACATGACTATTTGTTCTGTGAGTTCTATCAAGAGAAAAG 852

RESULT 8
ACC87557
ID ACC87557 standard; cDNA; 1016 BP.
XX
AC ACC87557;
XX
DT 05-AUG-2003 (first entry)
XX
DE Human secreted polypeptide PR0702-encoding cDNA, SEQ ID NO:99.
XX
KW Human; PRO; secreted protein; transmembrane protein;
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnery; gene therapy; gene; ss.
XX
CS Homo sapiens.
XX
PN US2003027278-A1.
XX
PD
XX
PF 06-FEB-2003.
XX
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 Query Match 81.6%; Score 678; DB 7; Length 1016;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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 Db 22 ATGAATGGCTTTTGATCCTTCTCGAAGAAACCAATTTATCCTCTCTGTACTATTCTT 81
 QY 61 TTGCAATTTCAGAGTCTGGGTCTGGATTTGATAGCGCTCTACCGCTGAAGTCTGTGCC 120
 Db 82 TTGCAATTTCAGAGTCTGGGTCTGGATTTGATAGCGCTCTACCGCTGAAGTCTGTGCC 141
 QY 121 ACACACAAATTTCCACGAGCACCACCAAGAGAGATGATGGTGAAGAAAGAGATCCAGAGAA 180
 Db 142 ACACACAAATTTCCACGAGCACCACCAAGAGAGATGATGGTGAAGAAAGAGATCCAGAGAA 201
 QY 181 GAGGAAAGCATGCAAAAGTGGGACGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 240
 Db 202 GAGGAAAGCATGCAAAAGTGGGACGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 261
 QY 241 CATATGGGAGATCGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGAGGGGTGACAAA 300
 Db 262 CATATGGGAGATCAGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGAGGGGTGACAAA 321
 QY 301 GGGGAAAGGTTTGTCTGGATACCTGGAGAAAGGCGGCGGCGGCGGCGGCGGCGGCTGTGAT 360
 Db 322 GGGGAAAGGTTTGTCTGGATACCTGGAGAAAGGCGGCGGCGGCGGCGGCGGCGGCTGTGAT 381
 QY 361 TGTGAAGATACCGGCAATTTGTGGCAACTGGATATTAGTATTGCGCGGCGGCGGCGGCGGCT 420
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 QY 601 RAGAGTGGCTTCTTCGGGTGTTTCATTGGCGTGAATGACCTTGAAGGGAGGACAGTAC 660
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DT 05-AUG-2003 (first entry)
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KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
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KW liver; drug screening; transgenic animal; genetic analysis;
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QY	121	ACACACACAAATTCACAGGACCCAAAGGAGATGATGTTGAAAAAGGAGATCCAGAGAA	180
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QY	721	GACCCCTATGTCATGAGGACTGTGGAGATCTGAGCTCTGGCAGATGGAATGACACA	780
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QY	781	GAGTGCCATCTTACCATGTACTTTGCTGTGAGTTTCATCAAGAGAAAAAG	831
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KW	tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;		
KW	tissue typing.		
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XX	US2003040070-A1.		
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PR	10-JUN-1998;	98US-0088740P.	PR	16-SEP-1998;	98US-0100662P.
PR	10-JUN-1998;	98US-0088811P.	PR	16-SEP-1998;	98US-0100664P.
PR	10-JUN-1998;	98US-0088824P.	PR	16-SEP-1998;	98US-0101751P.
PR	10-JUN-1998;	98US-0088825P.	PR	17-SEP-1998;	98US-0100683P.
PR	10-JUN-1998;	98US-0088826P.	PR	17-SEP-1998;	98US-0100684P.
PR	11-JUN-1998;	98US-0088861P.	PR	17-SEP-1998;	98US-0100684P.

Query Match				81.6%;	Score 678;	DB 7;	Length 1016;
Best Local Similarity				99.6%;	Pred. No. 0;		
Matches 828;				Conservative	0;	Mismatches 3;	Indels 0; Gaps 0;
QY	1	ATGAATGGCTTTGCATCCTTGTCTTCGAAAGAACCAATTTATCCTCCTGGTACTATTTCTT	60				
DB	22	ATGAATGGCTTTGCATCCTTGTCTTCGAAAGAACCAATTTATCCTCCTGGTACTATTTCTT	81				
QY	61	TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGCTCTACCGCTGAAGTCTGTGCC	120				
DB	82	TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGCTCTACCGCTGAAGTCTGTGCC	141				
QY	121	ACACACACAAATTTACACAGACCCAAAGAGAGATGATGGTGAATAAAGAGAGATCCAGAGAA	180				
DB	142	ACACACACAAATTTACACAGACCCAAAGAGAGATGATGGTGAATAAAGAGATCCAGAGAA	201				
QY	181	GAGGAAAGCATGGCAAAGTGGGACGCAATGGGGCCGAAAGGAATTAAGAGAGAACTGGGT	240				
DB	202	GAGGAAAGCATGGCAAAGTGGGACGCAATGGGGCCGAAAGGAATTAAGAGAGAACTGGGT	261				
QY	241	GATATGGAGATCGGGGCAATATTGGCAAGCTGGGCCCAATGGGAAGAGGGTGACAA	300				
DB	262	GATATGGAGATCAGGGCAATATTGGCAAGCTGGGCCCAATGGGAAGAGGGTGACAA	321				
QY	301	GGGGAAAAAGGTTTGTCTTGGATACTCGGAAAAAGGCAAGCAGGTACTGTCTGTGAT	360				
DB	322	GGGGAAAAAGGTTTGTCTTGGATACTCGGAAAAAGGCAAGCAGGTACTGTCTGTGAT	381				
QY	361	TGTGGAGATACCGGAATTTTGTGGCAACTGGATATTAGTATTGCCCGGCTCAAGACA	420				
DB	382	TGTGGAGATACCGGAATTTTGTGGCAACTGGATATTAGTATTGTCTGGCTCAAGACA	441				
QY	421	TCTATGAAGTTTGTCAAGAAATGTATAGCAGGGATTAGGGAAACTGAAAGAGAAATTTCTAC	480				
DB	442	TCTATGAAGTTTGTCAAGAAATGTATAGCAGGGATTAGGGAAACTGAAAGAGAAATTTCTAC	501				
QY	481	TACATCTGTCAGAGAGACAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGGGGT	540				
DB	502	TACATCTGTCAGAGAGAGAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGGGGT	561				
QY	541	GGAAATGCTAGGCATGCCCAAGGATGAAGCTGCCAACACACTCATCTGCTGACTATGTTGCC	600				
DB	562	GGAAATGCTAGGCATGCCCAAGGATGAAGCTGCCAACACACTCATCTGCTGACTATGTTGCC	621				
QY	601	AAGAGTGGCTTTCTCGGGTGTTCATTTGGCGTGAATGACCTTGAAGGGAGGGACAGTAC	660				
DB	622	AAGAGTGGCTTTCTCGGGTGTTCATTTGGCGTGAATGACCTTGAAGGGAGGGACAGTAC	681				
QY	661	ATGTTACAGACAACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGGAAACCCAGC	720				
DB	682	ATGTTCCACAGACAACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGGAAACCCAGC	741				
QY	721	GACCCCTATGTCATGAGAACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACA	780				
DB	742	GACCCCTATGTCATGAGAACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACA	801				
QY	781	GAGTGCCTATTACATGTACTTTTGTCTGTGAGTTTCATCAAGAGAAAAG	831				
DB	802	GAGTGCCTATTACATGTACTTTTGTCTGTGAGTTTCATCAAGAGAAAAG	852				

RESULT 12
ACA90292
ID ACA90292 standard; cdna; 1016 BP.
XX
AC ACA90292;
XX
DT 11-AUG-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO702 cdna.
XX
KW Human; gene therapy; tissue typing; tumour; chondrocyte proliferation;
KW chondrocyte differentiation; tumour necrosis factor-alpha release; ss;

KW	affinity purification; gene.
XX	Homo sapiens.
XX	US2003036147-A1.
XX	20-FEB-2003.
XX	02-JUL-2002; 2002US-00187741.
XX	18-SEP-1997; 97US-0059263P.
PR	18-SEP-1997; 97US-0059266P.
PR	17-OCT-1997; 97US-0062250P.
PR	21-OCT-1997; 97US-0063486P.
PR	24-OCT-1997; 97US-0083120P.
PR	24-OCT-1997; 97US-0083121P.
PR	28-OCT-1997; 97US-0063540P.
PR	28-OCT-1997; 97US-0063541P.
PR	28-OCT-1997; 97US-0063544P.
PR	28-OCT-1997; 97US-0063564P.
PR	29-OCT-1997; 97US-0063734P.
PR	31-OCT-1997; 97US-0083870P.
PR	31-OCT-1997; 97US-0084103P.
PR	13-NOV-1997; 97US-0065311P.
PR	21-NOV-1997; 97US-0066120P.
PR	24-NOV-1997; 97US-0066466P.
PR	24-NOV-1997; 97US-0066772P.
PR	11-DEC-1997; 97US-0069335P.
PR	12-DEC-1997; 97US-0089425P.
PR	17-DEC-1997; 97US-0089870P.
PR	18-DEC-1997; 97US-0086017P.
PR	10-MAR-1998; 98US-0077450P.
PR	11-MAR-1998; 98US-0077632P.
PR	11-MAR-1998; 98US-0077649P.
PR	20-MAR-1998; 98US-0078886P.
PR	20-MAR-1998; 98US-0078939P.
PR	27-MAR-1998; 98US-0079684P.
PR	27-MAR-1998; 98US-0079786P.
PR	31-MAR-1998; 98US-0080107P.
PR	31-MAR-1998; 98US-0080194P.
PR	01-APR-1998; 98US-0080327P.
PR	01-APR-1998; 98US-0080333P.
PR	08-APR-1998; 98US-0081049P.
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PR	15-APR-1998; 98US-0081838P.
PR	21-APR-1998; 98US-0082568P.
PR	21-APR-1998; 98US-0082569P.
PR	22-APR-1998; 98US-0082704P.
PR	22-APR-1998; 98US-0082797P.
PR	28-APR-1998; 98US-0083495P.
PR	29-APR-1998; 98US-0083496P.
PR	29-APR-1998; 98US-0083499P.
PR	29-APR-1998; 98US-0083559P.
PR	05-MAY-1998; 98US-0084366P.
PR	06-MAY-1998; 98US-0084414P.
PR	07-MAY-1998; 98US-0084639P.
PR	07-MAY-1998; 98US-0084640P.
PR	07-MAY-1998; 98US-0084643P.
PR	15-MAY-1998; 98US-0085579P.
PR	15-MAY-1998; 98US-0085580P.
PR	15-MAY-1998; 98US-0085582P.
PR	18-MAY-1998; 98US-0086023P.
PR	22-MAY-1998; 98US-0086332P.
PR	22-MAY-1998; 98US-0086486P.
PR	28-MAY-1998; 98US-0087098P.
PR	28-MAY-1998; 98US-0087208P.
PR	02-JUN-1998; 98US-0087609P.
PR	02-JUN-1998; 98US-0087759P.
PR	03-JUN-1998; 98US-0087827P.
PR	04-JUN-1998; 98US-0088025P.

QY 361 TCTGGAAGATCCGGAATTTGTTGGCAACTGATATTAGTATTCGCCGCTCAAGACA 420
 Db 382 TGTGGAAGATCCGGAATTTGTTGGCAACTGATATTAGTATTCGCCGCTCAAGACA 441
 QY 421 TCTATGAAGTTTGTCAAGATGTGATAGCAGGATTAGGGAATCTGAAGAGAAATTTCTAC 480
 Db 442 TCTATGAAGTTTGTCAAGATGTGATAGCAGGATTAGGGAATCTGAAGAGAAATTTCTAC 501
 QY 481 TACATCGTGCAGGAGAGAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGGGT 540
 Db 502 TACATCGTGCAGGAGAGAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGGGT 561
 QY 541 GGAATGCTAGCATCCCAAGGATGAAGCTGCCAACACACTCATCGCTGACTATGTTGCC 600
 Db 562 GGAATGCTAGCATCCCAAGGATGAAGCTGCCAACACACTCATCGCTGACTATGTTGCC 621
 QY 601 AAGAGTGGCTTTTCGGGTGTTTCATTTGGCGTGAATGACCTTGAAGGGAGGACAGTAC 660
 Db 622 AAGAGTGGCTTTTCGGGTGTTTCATTTGGCGTGAATGACCTTGAAGGGAGGACAGTAC 681
 QY 661 ATGTTTCAAGACAACTCCCACTGAGAACTATAGCAACTGGAATGAGGGGAACCCAGC 720
 Db 682 ATGTTTCAAGACAACTCCCACTGAGAACTATAGCAACTGGAATGAGGGGAACCCAGC 741
 QY 721 GACCCCTATGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGCAGATGGAATGACACA 780
 Db 742 GACCCCTATGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGCAGATGGAATGACACA 801
 QY 781 GAGTGCATCTTACCATTGCTGTTGCTGAGTTCATCAAGAGAAAAG 831
 Db 802 GAGTGCATCTTACCATTGCTGTTGCTGAGTTCATCAAGAGAAAAG 852

RESULT 13
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 ID ACC89399 standard; cdna; 1016 bp.
 AC ACC89399;
 XX
 AC ACC89399;
 XX
 DT 11-AUG-2003 (first entry)
 DE
 DE Human secreted polypeptide PRO702-encoding cdna, SEQ ID NO:99.
 XX
 XX Human; PRO; secreted protein; transmembrane protein;
 KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
 KW chondrocyte; proliferation; differentiation; cartilage disorder;
 KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
 KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
 KW liver; drug screening; transgenic animal; genetic analysis;
 KW antiarthritic; vulnery; gene therapy; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FN US2003027264-A1.
 XX
 PD 06-FEB-2003.
 XX
 XX 18-JUN-2002; 2002US-00174579.
 PF
 PF 18-SEP-1997; 97US-0059263P.
 XX
 PR 18-SEP-1997; 97US-0059263P.
 PR 17-OCT-1997; 97US-0062250P.
 PR 21-OCT-1997; 97US-0063486P.
 PR 24-OCT-1997; 97US-0063120P.
 PR 24-OCT-1997; 97US-0063121P.
 PR 28-OCT-1997; 97US-0063540P.
 PR 28-OCT-1997; 97US-0063541P.
 PR 28-OCT-1997; 97US-0063544P.
 PR 28-OCT-1997; 97US-0063564P.
 PR 29-OCT-1997; 97US-0063734P.
 PR 31-OCT-1997; 97US-0063870P.
 PR 31-OCT-1997; 97US-0064103P.
 PR 13-NOV-1997; 97US-0065311P.

PR 21-NOV-1997; 97US-0066120P.
 PR 24-NOV-1997; 97US-0066466P.
 PR 11-DEC-1997; 97US-0069335P.
 PR 12-DEC-1997; 97US-0069425P.
 PR 17-DEC-1997; 97US-0069870P.
 PR 18-DEC-1997; 97US-0068017P.
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 PR 20-MAR-1998; 98US-0078939P.
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 PR 27-MAR-1998; 98US-0079786P.
 PR 31-MAR-1998; 98US-0080107P.
 PR 31-MAR-1998; 98US-0080194P.
 PR 01-APR-1998; 98US-0080327P.
 PR 01-APR-1998; 98US-0080333P.
 PR 08-APR-1998; 98US-0081049P.
 PR 08-APR-1998; 98US-0081070P.
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 PR 22-APR-1998; 98US-0082704P.
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 PR 05-MAY-1998; 98US-0084366P.
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 PR 07-MAY-1998; 98US-0084639P.
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 PR 15-MAY-1998; 98US-0085582P.
 PR 15-MAY-1998; 98US-0085700P.
 PR 18-MAY-1998; 98US-0086023P.
 PR 22-MAY-1998; 98US-0086392P.
 PR 22-MAY-1998; 98US-0086486P.
 PR 28-MAY-1998; 98US-0087098P.
 PR 28-MAY-1998; 98US-0087208P.
 PR 02-JUN-1998; 98US-0087609P.
 PR 03-JUN-1998; 98US-0087759P.
 PR 04-JUN-1998; 98US-0087827P.
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 PR 10-JUN-1998; 98US-0088722P.
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 PR 16-JUN-1998; 98US-0089512P.
 PR 16-JUN-1998; 98US-0089514P.
 PR 17-JUN-1998; 98US-0089538P.

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PR	23-SEP-1998;	98US-0101477P.
PR	24-SEP-1998;	98US-0101738P.
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PR	25-SEP-1998;	98US-0101786P.
PR	29-SEP-1998;	98US-0102207P.
PR	29-SEP-1998;	98US-0102240P.
PR	29-SEP-1998;	98US-0102330P.
PR	30-SEP-1998;	98US-0102331P.
PR	30-SEP-1998;	98US-0102487P.
PR	30-SEP-1998;	98US-0102570P.
PR	30-SEP-1998;	98US-0102571P.
PR	01-OCT-1998;	98US-0102684P.
PR	01-OCT-1998;	98US-0102687P.

Query Match 81.6%; Score 678; DB 7; Length 1016;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	1	ATGTAATGCCTTTGCATCCTTGTCTTCGAAGAACCAATTTATCCTCGTGACTATTCTT	60
Dd	22	ATGTAATGCCTTTGCATCCTTGTCTTCGAAGAACCAATTTATCCTCGTGACTATTCTT	81
Qy	61	TTGGCAAATTCAGAGTCTGGGTCGTGATATTGATAGCGCTCCTACCGCTGAAGTCTGTGCC	120
Dd	82	TTGCAAATTCAGAGTCTGGGTCGTGATATTGATAGCGCTCCTACCGCTGAAGTCTGTGCC	141
Qy	121	ACACACACAATTTCCACAGAGCCCCAAGAAGATGATGTTGAJAAAAAGAGATCCAGGAGAA	180
Dd	142	ACACACACAATTTCCACAGAGCCCCAAGAAGATGATGTTGAJAAAAAGAGATCCAGGAGAA	201
Qy	181	GAGGAAAAGCATGCCAAATGCGACGCGATGGGSCCGAAAGGAATTAJAAAGGAGAACTGGGT	240
Dd	202	GAGGAAAAGCATGCCAAATGCGACGCGATGGGSCCGAAAGGAATTAJAAAGGAGAACTGGGT	261
Qy	241	GATATGGAGATCGGGGCAATATTGGCACAGACTGGGCCCATTTGGGAAAGAGGTGACAAA	300
Dd	262	GATATGGAGATCATAGGCAATATTGGCACAGACTGGGCCCATTTGGGAAAGAGGTGACAAA	321
Qy	301	GGGAAAAGGTTTGTCTTGAATACTGGAGAAAAGGCAAGCAGGACTGTCTGTGAT	360
Dd	322	GGGAAAAGGTTTGTCTTGAATACTGGAGAAAAGGCAAGCAGGACTGTCTGTGAT	381
Qy	361	TGTGGAAGATACCGBAAATTTGTTGGACAACCTGATATTAATGATTGCCCGCTCAAGACA	420
Dd	382	TGTGGAAGATACCGBAAATTTGTTGGACAACCTGATATTAATGATTGCCCGCTCAAGACA	441
Qy	421	TCTATGAAGTTTGTCAAGATGTATAGCAGGGATTTAGGGAACCTGAAGAGAAATTTCTAC	480
Dd	442	TCTATGAAGTTTGTCAAGATGTATAGCAGGGATTTAGGGAACCTGAAGAGAAATTTCTAC	501
Qy	481	TACATCGTGCAGGAAGAGAAGAACTACAGGGAATCCCTAAACCACTGCAGGATTCGGGT	540
Dd	502	TACATCGTGCAGGAAGAGAAGAACTACAGGGAATCCCTAAACCACTGCAGGATTCGGGT	561
Qy	541	GGATGCTTAGCCATGCCCAAGGATGAAGCTGCCAACACACACTCATCGCTGACTGTGTGCC	600
Dd	562	GGATGCTTAGCCATGCCCAAGGATGAAGCTGCCAACACACACTCATCGCTGACTGTGTGCC	621
Qy	601	AAGATGCTTCTTTTGGGFTTTCATTGGCGTGAATGACCTTGAAGAGGAGGACAGTAC	660
Dd	622	AAGATGCTTCTTTTGGGFTTTCATTGGCGTGAATGACCTTGAAGAGGAGGAGACAGTAC	681
Qy	661	ATGTTTCACAGACAACCTCCACTGCAAGACTATAGCAACTTGAATGAGGGGGAACCCAGC	720
Dd	682	ATGTTTCACAGACAACCTCCACTGCAAGACTATAGCAACTTGAATGAGGGGGAACCCAGC	741
Qy	721	GACCCCTATGGTCATGAGACTGTGTGGAGATGCTGAGCTCTGGCAGATGSAATGACACA	780
Dd	742	GACCCCTATGGTCATGAGACTGTGTGGAGATGCTGAGCTCTGGCAGATGSAATGACACA	801

OY 781 GAGTCCGCTTACCATCTACTTCTGTGAGTTCTATCAAGAGAAAAG 831
DB |||||
802 GAGTCCGCTTACCATCTACTTCTGTGAGTTCTATCAAGAGAAAAG 852

RESULT 14

ACA98190
ID ACA98190 standard; cDNA; 1016 BP.

AC ACA98190;

XX
DT 25-JUL-2003 (first entry)

XX Novel human secreted and transmembrane protein PRO702 cDNA.

XX Human; secreted and transmembrane protein; PRO; transgenic animal;
KW knockout; chromosome identification; tissue typing; tumour;
KW chondrocyte proliferation; chondrocyte differentiation;
KW tumor necrosis factor-alpha release stimulator; gene; ss.

OS Homo sapiens.

XX US2003036144-A1.

PN
XX 20-FEB-2003.

PD
XX 01-JUL-2002; 2002US-00187601.

XX 18-SEP-1997; 97US-0059263P.

XX 18-SEP-1997; 97US-0059266P.

XX 17-OCT-1997; 97US-0062250P.

XX 21-OCT-1997; 97US-0063486P.

XX 24-OCT-1997; 97US-0063120P.

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XX 28-OCT-1997; 97US-0063540P.

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PR 07-MAY-1998; 98US-0084639P.
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PR 02-JUN-1998; 98US-0087609P.
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5	19	2.3	5067	3	US-09-142-334-23
6	19	2.3	5129	4	US-09-566-921-107
7	18	2.2	1272	4	US-09-252-991A-15539
8	18	2.2	1618	4	US-09-489-847-82
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ALIGNMENTS

RESULT 1
US-09-620-312D-110
; Sequence 110, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yungqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP28
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
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; LENGTH: 6674
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1312)..(6330)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(6674)
; OTHER INFORMATION: n = a,t,c or g
US-09-620-312D-110

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Best Local Similarity 100.0%; Pred. No. 1.9; 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0;

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DB 2188 GGTGACAAAGGGGAAAAAGG 2207

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US-09-620-312D-110/c
; Sequence 110, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Felyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Fing
; APPLICANT: Ma, Yungqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: NO. 6569662el Nucleic Acids and
; FILE REFERENCE: Polypeptides
; CURRENT APPLICATION NUMBER: US/09/620,312D
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 110
; LENGTH: 6674
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1312) .. (6330)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1) .. (6674)
; OTHER INFORMATION: n = a,t,c or g
US-09-620-312D-110

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Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3

US-08-793-126-2
; Sequence 2, Application US/08793126
; Patent No. 5849297
; GENERAL INFORMATION:
; APPLICANT: Harrison, Richard Alexander
; APPLICANT: Faries, Charles Timothy
; TITLE OF INVENTION: MODIFIED HUMAN C3 PROTEINS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HALE AND DORR LLP
; STREET: 60 State Street
; CITY: Boston

STATE: MA
COUNTRY: United States of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,126
FILING DATE: 07-FEB-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Hollie L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 102286.377
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5056 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-793-126-2

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Best Local Similarity 100.0%; Pred. No. 6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 766 AGAGAAATTCCTACTACATC 784

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; Sequence 2, Application US/09132271
; Patent No. 6221657
; GENERAL INFORMATION:
; APPLICANT: Harrison, Richard Alexander
; APPLICANT: Faries, Charles Timothy
; TITLE OF INVENTION: MODIFIED HUMAN C3 PROTEINS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HALE AND DORR LLP
; STREET: 60 State Street
; CITY: Boston
STATE: MA
COUNTRY: United States of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/132,271
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/793,126
FILING DATE: 07-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Hollie L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 102286.377
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 2:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 5056 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-132-271-2

Query Match      2.3%; Score 19; DB 3; Length 5056;
Best Local Similarity 100.0%; Pred. No. 6;
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DB 766 AGAGAAATTTCTACTACATC 784

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; Patent No. 6268485
; GENERAL INFORMATION:
; APPLICANT: Faries, Timothy C.
; TITLE OF INVENTION: Down-Regulation Resistant C3 Convertase
; FILE REFERENCE: 4-30443/A/IMU/PCT
; CURRENT APPLICATION NUMBER: US/09/142,334
; EARLIER FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: PCT/GB97/00603
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 23
; LENGTH: 5067
; TYPE: DNA
; ORGANISM: Homo sapiens
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Query Match      2.3%; Score 19; DB 3; Length 5067;
Best Local Similarity 100.0%; Pred. No. 6;
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DB 777 AGAGAAATTTCTACTACATC 795

RESULT 6
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; Sequence 107, Application US/09566921
; Patent No. 6682388
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.
; APPLICANT: Tingley, Debora W.
; APPLICANT: Edwards, Carla M.
; TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
; FILE REFERENCE: PA-0024 US
; CURRENT APPLICATION NUMBER: US/09/566,921
; CURRENT FILING DATE: 2000-03-05
; NUMBER OF SEQ ID NOS: 138
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; OTHER INFORMATION: Incyte ID No. 6582888 1000186.8
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Best Local Similarity 100.0%; Pred. No. 6;
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; Sequence 15539, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
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; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-15539

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Best Local Similarity 100.0%; Pred. No. 19;
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DB 684 GATAGCCGTCCTACCGCT 701

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; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
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; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-489-847-82

Query Match      2.2%; Score 18; DB 4; Length 1618;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 312 GAAGCGTCAAAAGGGGA 329

RESULT 9
US-09-593-995-10
; Sequence 10, Application US/09593995
; Patent No. 640688
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Gao, Zeren
; FILE OF INVENTION: HELICAL CYTOKINE ZALPHA33
; FILE REFERENCE: 99-38
; CURRENT APPLICATION NUMBER: US/09/593,995
; CURRENT FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: 60/139,121
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 20598
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-593-995-10

Query Match 2.2%; Score 18; DB 4; Length 20598;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 163 AAAGCAGATCCAGGAGAA 180
Db 3000 AAAGCAGATCCAGGAGAA 3017

RESULT 10
US-09-497-855A-40
; Sequence 40, Application US/09497855A
; Patent No. 6605432
; GENERAL INFORMATION:
; APPLICANT: Huang, Tim
; FILE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION
; FILE REFERENCE: UMO1523
; CURRENT APPLICATION NUMBER: US/09/497,855A
; CURRENT FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/120,592
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: 60/118,760
; PRIOR FILING DATE: 1999-02-05
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 40
; LENGTH: 161652
; TYPE: DNA
; ORGANISM: Homo sapiens;
US-09-497-855A-40

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Best Local Similarity 100.0%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 GCTGAAGTCTGTGCCACA 123
Db 10158 GCTGAAGTCTGTGCCACA 10175

RESULT 11
US-09-242-890-33
; Sequence 33, Application US/09242890
; Patent No. 6613887
; GENERAL INFORMATION:
; APPLICANT: Ogi, Kasuhiro
; APPLICANT: Onda, Haruo
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE
; FILE REFERENCE: 2417US0P

; CURRENT APPLICATION NUMBER: US/09/242,890
; CURRENT FILING DATE: 1999-02-28
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-08-10
; PRIOR APPLICATION NUMBER: JP 8-240880
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: JP 8-318049
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: JP 9-135633
; PRIOR FILING DATE: 1997-05-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE:
; SEQ ID NO 33
; LENGTH: 102
; TYPE: DNA
; ORGANISM: Rat
US-09-242-890-33

Query Match 2.0%; Score 17; DB 4; Length 102;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 TCTGGGTCTGGATATTG 91
Db 65 TCTGGGTCTGGATATTG 81

RESULT 12
US-09-621-976-132
; Sequence 132, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET 054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 132
; LENGTH: 477
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 124..477
; NAME/KEY: sig_peptide
; LOCATION: 124..273
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 6
; OTHER INFORMATION: seq LFTLLSLMELFP/AE
; NAME/KEY: misc_feature
; LOCATION: 394
; OTHER INFORMATION: n=a, g, c or t
US-09-621-976-132

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Best Local Similarity 100.0%; Pred. No. 60;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 GAAGAGGGAAGCATGG 194
Db 307 GAAGAGGGAAGCATGG 323

RESULT 13
US-09-242-890-29
; Sequence 29, Application US/09242890
; Patent No. 6613887
; GENERAL INFORMATION:
; APPLICANT: Ogi, Kasuhiro

; APPLICANT: Onda, Haruo
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE
; FILE REFERENCE: 2417USOP
; CURRENT APPLICATION NUMBER: US/09/242,890
; CURRENT FILING DATE: 1999-02-28
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-08-10
; PRIOR APPLICATION NUMBER: JP 8-240880
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: JP 8-318049
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: JP 9-135633
; PRIOR FILING DATE: 1997-05-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE:
; SEQ ID NO 29
; LENGTH: 672
; TYPE: DNA
; ORGANISM: Rat
US-09-242-890-29

Query Match 2.0%; Score 17; DB 4; Length 672;
Best Local Similarity 100.0%; Fred. No. 61;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 TCTGGGCTCTGGATATTG 91
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Db 65 TCTGGGCTCTGGATATTG 81

RESULT 14

US-09-489-039A-686/c
; Sequence 686, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 686
; LENGTH: 837
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-686

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Best Local Similarity 100.0%; Fred. No. 61;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 289 AAGGGTGACAAAGGGGA 305
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Db 102 AAGGGTGACAAAGGGGA 86

RESULT 15

US-09-401-064-329/c
; Sequence 329, Application US/09401064
; Patent No. 6623923
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeline Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE

; FILE REFERENCE: 210121.471C2
; CURRENT APPLICATION NUMBER: US/09/401,064
; CURRENT FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 371
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 329
; LENGTH: 854
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(854)
; OTHER INFORMATION: n = A,T,C or G
US-09-401-064-329

Query Match 2.0%; Score 17; DB 4; Length 854;
Best Local Similarity 100.0%; Fred. No. 61;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 TGTGATTGTGGAAGATA 371
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Db 573 TGTGATTGTGGAAGATA 557

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OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 18:44:32 ; Search time 361 Seconds
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Gapop 60.0 , Gapext 60.0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	678	81.6	1016	9	Sequence 96, Appl
3	678	81.6	1016	9	Sequence 96, Appl
4	678	81.6	1016	9	Sequence 96, Appl
5	678	81.6	1016	9	Sequence 96, Appl
6	678	81.6	1016	10	US-09-978-189A-96
7	678	81.6	1016	10	US-09-978-608A-96
8	678	81.6	1016	10	US-09-978-191A-96
9	678	81.6	1016	10	US-09-978-403A-96
10	678	81.6	1016	10	US-09-978-564A-96
11	678	81.6	1016	10	US-09-978-833A-96
12	678	81.6	1016	10	US-09-978-191A-96
13	678	81.6	1016	10	US-09-978-824A-96
14	678	81.6	1016	10	US-09-978-585A-96
15	678	81.6	1016	10	US-09-978-423A-96

16	678	81.6	1016	10	US-09-978-193A-96
17	678	81.6	1016	10	US-09-978-830A-96
18	678	81.6	1016	10	US-09-978-757A-96
19	678	81.6	1016	10	US-09-978-187B-96
20	678	81.6	1016	10	US-09-978-643A-96
21	678	81.6	1016	10	US-09-978-375A-96
22	678	81.6	1016	10	US-09-978-298A-96
23	678	81.6	1016	10	US-09-978-188A-96
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26	678	81.6	1016	10	US-09-978-829A-96
27	678	81.6	1016	10	US-09-978-299A-96
28	678	81.6	1016	10	US-09-978-544A-96
29	678	81.6	1016	10	US-09-978-665A-96
30	678	81.6	1016	10	US-09-978-802A-96
31	678	81.6	1016	12	US-10-164-749A-96
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33	678	81.6	1016	12	US-10-199-670-99
34	678	81.6	1016	12	US-10-201-858-99
35	678	81.6	1016	13	US-10-052-586-99
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39	678	81.6	1016	14	US-10-173-706-99
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44	678	81.6	1016	14	US-10-176-913-99
45	678	81.6	1016	14	US-10-180-552-99

ALIGNMENTS

RESULT 1
US-09-978-295A-96
; Sequence 96, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Pao, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630F1C11
; CURRENT APPLICATION NUMBER: US/09/978,295A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585

1 PRIOR FILING DATE: 2001-07-30
2 PRIOR APPLICATION NUMBER: 60/062250
3 PRIOR FILING DATE: 1997-10-17
4 PRIOR APPLICATION NUMBER: 60/064249
5 PRIOR FILING DATE: 1997-11-03
6 PRIOR APPLICATION NUMBER: 60/065311
7 PRIOR FILING DATE: 1997-11-13
8 PRIOR APPLICATION NUMBER: 60/066364
9 PRIOR FILING DATE: 1997-11-21
10 PRIOR APPLICATION NUMBER: 60/077450
11 PRIOR FILING DATE: 1998-03-10
12 PRIOR APPLICATION NUMBER: 60/077632
13 PRIOR FILING DATE: 1998-03-11
14 PRIOR APPLICATION NUMBER: 60/077641
15 PRIOR FILING DATE: 1998-03-11
16 PRIOR APPLICATION NUMBER: 60/077649
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18 PRIOR APPLICATION NUMBER: 60/077791
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20 PRIOR APPLICATION NUMBER: 60/078004
21 PRIOR FILING DATE: 1998-03-13
22 PRIOR APPLICATION NUMBER: 60/078886
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24 PRIOR APPLICATION NUMBER: 60/078936
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26 PRIOR APPLICATION NUMBER: 60/078910
27 PRIOR FILING DATE: 1998-03-20
28 PRIOR APPLICATION NUMBER: 60/078939
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30 PRIOR APPLICATION NUMBER: 60/079294
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33 PRIOR FILING DATE: 1998-03-26
34 PRIOR APPLICATION NUMBER: 60/079664
35 PRIOR FILING DATE: 1998-03-27
36 PRIOR APPLICATION NUMBER: 60/079689
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38 PRIOR APPLICATION NUMBER: 60/079663
39 PRIOR FILING DATE: 1998-03-27
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45 PRIOR FILING DATE: 1998-03-30
46 PRIOR APPLICATION NUMBER: 60/079923
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50 PRIOR APPLICATION NUMBER: 60/080107
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56 PRIOR APPLICATION NUMBER: 60/080327
57 PRIOR FILING DATE: 1998-04-01
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 / PRIOR FILING DATE: 1998-05-15
 / PRIOR APPLICATION NUMBER: 60/085704
 / PRIOR FILING DATE: 1998-05-15
 / PRIOR APPLICATION NUMBER: 60/085697

Query Match 81.6%; Score 678; DB 9; Length 1016;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGAATGGCTTTGCATCCTTCTCGAAGAAACCAATTTATCTCTCGTACTATTCTTT 60

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QY 61 TTGCAATTTCAGACTCTGGGCTTGGATATTGATAGCGCTCTACCGCTGAAGTCTGTGCC 120

Db 82 TTGCAATTCAGAGTCTGGTCTGGATATGATAGCCGTCTACCGCTGAAGTCTGTGCC 141
 QY 121 ACACACAAATTCACAGGACCCAAAGGAGATGATGTTGAAAAGGAGATCCAGAGAA 180
 Db 142 ACACACAAATTCACAGGACCCAAAGGAGATGATGTTGAAAAGGAGATCCAGAGAA 201
 QY 181 GAGGGAAGAGTGGCAAGTGGAGCGATGGGCGGCAAGGAATTAAGGAGAACTGGGT 240
 Db 202 GAGGGAAGAGTGGCAAGTGGAGCGATGGGCGGCAAGGAATTAAGGAGAACTGGGT 261
 QY 241 GATATGGAGATCGGGCAATATTTGGCAAGTGGGCGGCAATTTGGGAAGAGGCTGACAAA 300
 Db 262 GATATGGAGATCAGGCAATATTTGGCAAGTGGGCGGCAATTTGGGAAGAGGCTGACAAA 321
 QY 301 GGGGAAGAGTGGTCTGGATACCTGGAGAAAAGCAAGCAGTACTGCTGTGAT 360
 Db 322 GGGGAAGAGTGGTCTGGATACCTGGAGAAAAGCAAGCAGTACTGCTGTGAT 381
 QY 361 TGTGGAAGATACCGGAATTTGTTGGCAACTGATATTAGTATTCGCCGCTCAAGACA 420
 Db 382 TGTGGAAGATACCGGAATTTGTTGGCAACTGATATTAGTATTCGCCGCTCAAGACA 441
 QY 421 TCTATGAAGTTGTCAAGATGTGATAGCAGGATTAGGGAACCTGAAGAGAATTTCTAC 480
 Db 442 TCTATGAAGTTGTCAAGATGTGATAGCAGGATTAGGGAACCTGAAGAGAATTTCTAC 501
 QY 481 TACATCGTGCAGGAGAGAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGGGT 540
 Db 502 TACATCGTGCAGGAGAGAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGGGT 561
 QY 541 GGAATGCTAGCATCCCAAGGATGAAGCTGCCAACAACCTATCGCTGACTATGTTGCC 600
 Db 562 GGAATGCTAGCATCCCAAGGATGAAGCTGCCAACAACCTATCGCTGACTATGTTGCC 621
 QY 601 AAGAGTGGCTTTTCGGGTGTTTCATTGGGTGATGATCACTTGAAGGGAGGACAGTAC 660
 Db 622 AAGAGTGGCTTTTCGGGTGTTTCATTGGGTGATGATCACTTGAAGGGAGGACAGTAC 681
 QY 661 ATGTTACAGACAACACTCCACTCAGAACTATAGCAACTGGAATGAGGGGGAACCCAGC 720
 Db 682 ATGTTACAGACAACACTCCACTCAGAACTATAGCAACTGGAATGAGGGGGAACCCAGC 741
 QY 721 GACCCCTATGCTAGAGTCTGTGGAGTCTGAGCTCTGCGCATGGAATGACACA 780
 Db 742 GACCCCTATGCTAGAGTCTGTGGAGTCTGAGCTCTGCGCATGGAATGACACA 801
 QY 781 GAGTGGCATCTTACCATGTTTGTCTGTGAGTTTCATCAAGAGAAAAG 831
 Db 802 GAGTGGCATCTTACCATGTTTGTCTGTGAGTTTCATCAAGAGAAAAG 852

RESULT 3

US-09-978-192A-96
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 ; GENERAL INFORMATION:
 ; APPLICANT: Ashtenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Kljavin, Ivar J.
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 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James;
 ; APPLICANT: Paoni, Nicholas P.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2630P1C9
 ; CURRENT APPLICATION NUMBER: US/09/978,192A
 ; CURRENT FILING DATE: 2001-10-15
 ; PRIOR APPLICATION NUMBER: 09/918585
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 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 81.6%; Score 678; DB 9; Length 1016;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB	82	TTGCAAAATTCAGAGTCGGGTCTGGATATTGATAGCGCTCCTACCGCTGAAGTCTGTGCC	141
QY	121	ACACACAAATTTCCAGACCCCAAGAGAGATGGTGAAAGAGAGATCCAGAGAA	180
DB	142	ACACACAAATTTCCAGACCCCAAGAGAGATGGTGAAAGAGAGATCCAGAGAA	201
QY	181	GAGGAAAGCATGCAAGTGGGACCATGGGGCCGAAAGGAATTAAGAGAACTGGGT	240
DB	202	GAGGAAAGCATGCAAGTGGGACCATGGGGCCGAAAGGAATTAAGAGAACTGGGT	261
QY	241	GATATGGAGATCGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGAGGGTGACAA	300
DB	262	GATATGGAGATCAGGGCAATATTGGCAAGACTGGGGCCCATTTGGGAAGAGGGTGACAA	321
QY	301	GGGGAAGAGTTTGTGGTGAATACCTGGAGAAAGGCAAGCAGGTACTGTCTGTGAT	360
DB	322	GGGGAAGAGTTTGTGGTGAATACCTGGAGAAAGGCAAGCAGGTACTGTCTGTGAT	381
QY	361	TGTGGAAGATACCGGAAATTTGTGGCAACTGGATATTAGTATTCGCCGCTCAAGACA	420
DB	382	TGTGGAAGATACCGGAAATTTGTGGCAACTGGATATTAGTATTCGCCGCTCAAGACA	441
QY	421	TCTATGAAGTTTGTCAAGATGTAGGAGGATTTAGGAACTGAAGAGAAATTTAC	480
DB	442	TCTATGAAGTTTGTCAAGATGTAGGAGGATTTAGGAACTGAAGAGAAATTTAC	501
QY	481	TACATCGTCAGGAAGAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGGGT	540

GENERAL INFORMATION:

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APPLICANT: Wood, William I.
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Query Match 81.6%; Score 678; DB 10; Length 1016;
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 Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	1	ATGAATGGCTTTTCATCTTCCTTCGAGAAACCAATTTATCTCTCTGGTACTATTTCTT	60
Db	22	ATGAATGGCTTTTCATCTTCCTTCGAGAAACCAATTTATCTCTCTGGTACTATTTCTT	81
QY	61	TTGCAATTCAGAGTCTGGTCTGGATTTGATAGCCCTCTACCGCTGAAGTCTGTGCC	120
Db	82	TTGCAATTCAGAGTCTGGTCTGGATTTGATAGCCCTCTACCGCTGAAGTCTGTGCC	141
QY	121	ACACACACAAATTTTCCACAGGACCCAAAGAGAGATGATGGTGAAGAGAGATCCAGAGAA	180
Db	142	ACACACACAAATTTTCCACAGGACCCAAAGAGAGATGATGGTGAAGAGAGATCCAGAGAA	201
QY	181	GAGGAAAGCATGGCAATGGGACGATGGGCGGAAAGAAATTAAGAGAGAACTGGGT	240
Db	202	GAGGAAAGCATGGCAATGGGACGATGGGCGGAAAGAAATTAAGAGAGAACTGGGT	261

QY	241	GATATGGAGATCGGGCAATATTGGCAAGACTGGGCCCATTCGGAAGAGAGGCTGACAA	300
Db	262 <th>GATATGGAGATCAGGGCAATATTGGCAAGACTGGGCCCATTCGGAAGAGAGGCTGACAA</th> <th>321</th>	GATATGGAGATCAGGGCAATATTGGCAAGACTGGGCCCATTCGGAAGAGAGGCTGACAA	321
QY	301 <th>GGGAAAAAGGTTTCTTGGAAATACCTGGAGAAAAAGGCAAGAGAGTACTGTCTGTGAT</th> <th>360</th>	GGGAAAAAGGTTTCTTGGAAATACCTGGAGAAAAAGGCAAGAGAGTACTGTCTGTGAT	360
Db	322 <th>GGGAAAAAGGTTTCTTGGAAATACCTGGAGAAAAAGGCAAGAGAGTACTGTCTGTGAT</th> <th>381</th>	GGGAAAAAGGTTTCTTGGAAATACCTGGAGAAAAAGGCAAGAGAGTACTGTCTGTGAT	381
QY	361 <th>TGTGAGATATACCGGAAATTTTGGGAACTAGTATTTAGTATTTGCTCGGCTCAAGACA</th> <th>420</th>	TGTGAGATATACCGGAAATTTTGGGAACTAGTATTTAGTATTTGCTCGGCTCAAGACA	420
Db	382 <th>TGTGAGATATACCGGAAATTTTGGGAACTAGTATTTAGTATTTGCTCGGCTCAAGACA</th> <th>441</th>	TGTGAGATATACCGGAAATTTTGGGAACTAGTATTTAGTATTTGCTCGGCTCAAGACA	441
QY	421 <th>TCTATGAAGTTTGTCAAGAAATGTGATAGCAGGATAGGGAATCAAGAGAAATTTCTAC</th> <th>480</th>	TCTATGAAGTTTGTCAAGAAATGTGATAGCAGGATAGGGAATCAAGAGAAATTTCTAC	480
Db	442 <th>TCTATGAAGTTTGTCAAGAAATGTGATAGCAGGATAGGGAATCAAGAGAAATTTCTAC</th> <th>501</th>	TCTATGAAGTTTGTCAAGAAATGTGATAGCAGGATAGGGAATCAAGAGAAATTTCTAC	501
QY	481 <th>TACATCGTGCAGGAGAGAGAACTACAGGGAATCCCTACCCACTGCAGGATTCGGGT</th> <th>540</th>	TACATCGTGCAGGAGAGAGAACTACAGGGAATCCCTACCCACTGCAGGATTCGGGT	540
Db	502 <th>TACATCGTGCAGGAGAGAGAACTACAGGGAATCCCTACCCACTGCAGGATTCGGGT</th> <th>561</th>	TACATCGTGCAGGAGAGAGAACTACAGGGAATCCCTACCCACTGCAGGATTCGGGT	561
QY	541 <th>GGAATGTAGCCATGCCCAAGGATGAAGCTGCCAACAACACTCATCTGCTGACTATGTGCC</th> <th>600</th>	GGAATGTAGCCATGCCCAAGGATGAAGCTGCCAACAACACTCATCTGCTGACTATGTGCC	600
Db	562 <th>GGAATGTAGCCATGCCCAAGGATGAAGCTGCCAACAACACTCATCTGCTGACTATGTGCC</th> <th>621</th>	GGAATGTAGCCATGCCCAAGGATGAAGCTGCCAACAACACTCATCTGCTGACTATGTGCC	621
QY	601 <th>AAGATGGCTTCTTTTCGGGTCTTCATTTGGCGTGAATGACCTTGAAGGGAGGACAGTAC</th> <th>660</th>	AAGATGGCTTCTTTTCGGGTCTTCATTTGGCGTGAATGACCTTGAAGGGAGGACAGTAC	660
Db	622 <th>AAGATGGCTTCTTTTCGGGTCTTCATTTGGCGTGAATGACCTTGAAGGGAGGACAGTAC</th> <th>681</th>	AAGATGGCTTCTTTTCGGGTCTTCATTTGGCGTGAATGACCTTGAAGGGAGGACAGTAC	681
QY	661 <th>ATGTTTCAGACAAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGAAACCAGC</th> <th>720</th>	ATGTTTCAGACAAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGAAACCAGC	720
Db	682 <th>ATGTTTCAGACAAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGAAACCAGC</th> <th>741</th>	ATGTTTCAGACAAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGAAACCAGC	741
QY	721 <th>GACCCCTATGCTATGAGGACTGTGAGATGCTGAGTCTGCGAGATGGAATGACACA</th> <th>780</th>	GACCCCTATGCTATGAGGACTGTGAGATGCTGAGTCTGCGAGATGGAATGACACA	780
Db	742 <th>GACCCCTATGCTATGAGGACTGTGAGATGCTGAGTCTGCGAGATGGAATGACACA</th> <th>801</th>	GACCCCTATGCTATGAGGACTGTGAGATGCTGAGTCTGCGAGATGGAATGACACA	801
QY	781 <th>GAGTGCCATCTTACCATGCTATTTGCTGCTGAGTTTCTCAAGAGAGAAAAAG</th> <th>831</th>	GAGTGCCATCTTACCATGCTATTTGCTGCTGAGTTTCTCAAGAGAGAAAAAG	831
Db	802 <th>GAGTGCCATCTTACCATGCTATTTGCTGCTGAGTTTCTCAAGAGAGAAAAAG</th> <th>852</th>	GAGTGCCATCTTACCATGCTATTTGCTGCTGAGTTTCTCAAGAGAGAAAAAG	852

RESULT 6
 US-09-978-608A-96
 ; Sequence 96, Application US/09978608A
 ; Publication No. US20030045462A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kijavini, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas P.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.

;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2630PIC22
;; CURRENT APPLICATION NUMBER: US/09/978,608A
;; NUMBER OF SEQ ID NOS: 624
;; Prior Application removed - See File Wrapper or Palm
;; SEQ ID NO 96
;; LENGTH: 1016
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-978-608A-96

Query Match 81.6%; Score 678; DB 10; Length 1016;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGAATGGCTTTGGCATCTCTCGTTCGAAGAAACCAATTTATCTCTCTGGTACTATTCTT 60
DB 22 ATGAATGGCTTTGGCATCTCTCGTTCGAAGAAACCAATTTATCTCTCTGGTACTATTCTT 81

QY 61 TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCGTCTTCCGCTGAAGTCTGTGCC 120
DB 82 TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCGTCTTCCGCTGAAGTCTGTGCC 141

QY 121 ACACACACAATTTCCACAGGACCCAAAGGAGATGATGTTGAAAAAGGAGATCCAGAGAA 180
DB 142 ACACACACAATTTCCACAGGACCCAAAGGAGATGATGTTGAAAAAGGAGATCCAGAGAA 201

QY 181 GAGGAAAGCATGCGAAAGTGGGACGATGGGCGGAAAGGAAATTAAGGAGAACTGGGT 240
DB 202 GAGGAAAGCATGCGAAAGTGGGACGATGGGCGGAAAGGAAATTAAGGAGAACTGGGT 261

QY 241 GATATGGAGATCGGGGCAATATTGGCAAGATCTGGGCCATTTGGGAAGAGGTGACAA 300
DB 262 GATATGGAGATCGGGGCAATATTGGCAAGATCTGGGCCATTTGGGAAGAGGTGACAA 321

QY 301 GGGGAAAAAGTTTCTGGGAATACCTGGGAAAAAGGCAAGAGTACTGTGTGAT 360
DB 322 GGGGAAAAAGTTTCTGGGAATACCTGGGAAAAAGGCAAGAGTACTGTGTGAT 381

QY 361 TGTGAAGATACCGGAATTTGTTGGCACTCTGATATTAGTATTCGCGCTCAAGACA 420
DB 382 TGTGAAGATACCGGAATTTGTTGGCACTCTGATATTAGTATTCGCGCTCAAGACA 441

QY 421 TCTATGAATTTGTCAAGATTTGATAGCGGATAGGAAATCTGAAGAGAAATTTCTAC 480
DB 442 TCTATGAATTTGTCAAGATTTGATAGCGGATAGGAAATCTGAAGAGAAATTTCTAC 501

QY 481 TACATCGTCAGGAGAGAGAACTCAGGGAATCCCTAACCCACTGCAGGATTCGGGT 540
DB 502 TACATCGTCAGGAGAGAGAACTCAGGGAATCCCTAACCCACTGCAGGATTCGGGT 561

QY 541 GGAATGTAGCATGCCAAGATGAAGTGCACACACTCATCGCTGACTATGTGTGCC 600
DB 562 GGAATGTAGCATGCCAAGATGAAGTGCACACACTCATCGCTGACTATGTGTGCC 621

QY 601 AAGAGTGGCTTCTTCGGGTCTCATTTGGGGTGAATGACCTTGAAAGGGAGGACAGTAC 660
DB 622 AAGAGTGGCTTCTTCGGGTCTCATTTGGGGTGAATGACCTTGAAAGGGAGGACAGTAC 681

QY 661 ATGTTTCACAGACAACACTCCACTGCAGAACTATAGCAACTGGGAATCAGGGGAAACCCAGC 720
DB 682 ATGTTTCACAGACAACACTCCACTGCAGAACTATAGCAACTGGGAATCAGGGGAAACCCAGC 741

QY 721 GACCCCTATGTCATGAGGACTGTGTGAGATGCTGAGCTCTGGCAGATGGAATGACACA 780
DB 742 GACCCCTATGTCATGAGGACTGTGTGAGATGCTGAGCTCTGGCAGATGGAATGACACA 801

QY 781 GAGTGCCTATCTACCATGACTTTGTCTGTGTGAGTTTCAAGAAAGAAAAG 831
DB 802 GAGTGCCTATCTACCATGACTTTGTCTGTGTGAGTTTCAAGAAAGAAAAG 852

RESULT 7
US-09-978-585A-96
; Sequence 96, Application US/09978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC15
; CURRENT APPLICATION NUMBER: US/09/978,585A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 96
; LENGTH: 1016
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-978-585A-96

Query Match 81.6%; Score 678; DB 10; Length 1016;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGAATGGCTTTGGCATCTCTCGTTCGAAGAAACCAATTTATCTCTCTGGTACTATTCTT 60
DB 22 ATGAATGGCTTTGGCATCTCTCGTTCGAAGAAACCAATTTATCTCTCTGGTACTATTCTT 81

QY 61 TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCGTCTTCCGCTGAAGTCTGTGCC 120
DB 82 TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCGTCTTCCGCTGAAGTCTGTGCC 141

QY 121 ACACACACAATTTCCACAGGACCCAAAGGAGATGATGTTGAAAAAGGAGATCCAGAGAA 180
DB 142 ACACACACAATTTCCACAGGACCCAAAGGAGATGATGTTGAAAAAGGAGATCCAGAGAA 201

QY 181 GAGGAAAGCATGCGAAAGTGGGACGATGGGCGGAAAGGAAATTAAGGAGAACTGGGT 240
DB 202 GAGGAAAGCATGCGAAAGTGGGACGATGGGCGGAAAGGAAATTAAGGAGAACTGGGT 261

QY 241 GATATGGAGATCGGGGCAATATTGGCAAGATCTGGGCCATTTGGGAAGAGGTGACAAA 300
DB 262 GATATGGAGATCGGGGCAATATTGGCAAGATCTGGGCCATTTGGGAAGAGGTGACAAA 321

QY 301 GGGGAAAAAGTTTCTGGGAATACCTGGGAAAAAGGCAAGAGTACTGTGTGAT 360
DB 322 GGGGAAAAAGTTTCTGGGAATACCTGGGAAAAAGGCAAGAGTACTGTGTGAT 381

QY 361 TGTGGAAGATACCGAAATTTGTTGGCAAACTGGATATTAGTATTGCCCGCTCAAGACA 420
 Db 382 TGTGGAAGATACCGAAATTTGTTGGCAAACTGGATATTAGTATTGCCCGCTCAAGACA 441
 QY 421 TCTATGAAGTTTGTCAAGAACTGTGTAGTACAGGGATTAGGAACTGAGAGAAATTTCTAC 480
 Db 442 TCTATGAAGTTTGTCAAGAACTGTGTAGTACAGGGATTAGGAACTGAGAGAAATTTCTAC 501
 QY 481 TACATGTCGACAGAAAGAGAACTACAGGAAATCCCTTAACCCACTCGAGATTTCGGGGT 540
 Db 502 TACATGTCGACAGAAAGAGAACTACAGGAAATCCCTTAACCCACTCGAGATTTCGGGGT 561
 QY 541 GGAATGCTAGCCATGCCCAAGATGAAGTCCCAACACATCATCGCTGACTATGTTGCC 600
 Db 562 GGAATGCTAGCCATGCCCAAGATGAAGTCCCAACACATCATCGCTGACTATGTTGCC 621
 QY 601 AAGAGTGGCTTTCTTTCCGGGTGTTTCAATTCGCGTGAATGACCTTGAAGGGAGGACAGTAC 660
 Db 622 AAGAGTGGCTTTCTTTCCGGGTGTTTCAATTCGCGTGAATGACCTTGAAGGGAGGACAGTAC 681
 QY 661 ATGTTCCACAGCAACACCTCCACTGACAGAACTATACCACTGGAATGAGGGAGCCAGC 720
 Db 682 ATGTTCCACAGCAACACCTCCACTGACAGAACTATACCACTGGAATGAGGGAGCCAGC 741
 QY 721 GACCCCTATGTCATGAGGACTGTGTGAGATGCTGAGCTCTGCGACATGGAATGACACA 780
 Db 742 GACCCCTATGTCATGAGGACTGTGTGAGATGCTGAGCTCTGCGACATGGAATGACACA 801
 QY 781 GAGTGCATCTTACCATGTACTTTCTGTGAGTTTCATCAAGAGAAAAG 831
 Db 802 GAGTGCATCTTACCATGTACTTTCTGTGAGTTTCATCAAGAGAAAAG 852

RESULT 8

US-09-978-191A-96
 ; Sequence 96, Application US/09978191A
 ; Publication No. US20030050239A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2630P1C4
 ; CURRENT APPLICATION NUMBER: US/09/978,191A
 ; CURRENT FILING DATE: 2001-10-15
 ; PRIOR APPLICATION NUMBER: 09/918585
 ; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/064249
 ; PRIOR FILING DATE: 1997-11-03
 ; PRIOR APPLICATION NUMBER: 60/065311
 ; PRIOR FILING DATE: 1997-11-13
 ; PRIOR APPLICATION NUMBER: 60/066364
 ; PRIOR FILING DATE: 1997-11-21
 ; PRIOR APPLICATION NUMBER: 60/077450
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 ; PRIOR APPLICATION NUMBER: 60/079294
 ; PRIOR FILING DATE: 1998-03-25
 ; PRIOR APPLICATION NUMBER: 60/079656
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; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 81.6%; Score 678; DB 10; Length 1016;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGAATGGCTTTTGCAATCCTTCTCGAAGAAACCAATTTATCTCTCTGGTACTATTTCIT 60
DB 22 ATGAATGGCTTTTGCAATCCTTCTCGAAGAAACCAATTTATCTCTCTGGTACTATTTCIT 81
QY 61 TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCGCTCTTACCGCTGAAGTCTGTGCC 120
DB 82 TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCGCTCTTACCGCTGAAGTCTGTGCC 141
QY 121 ACACACAAATTCACAGGACCCAAAGAGAGATGATGTGAAAAGAGAGATCCAGAGAA 180
DB 142 ACACACAAATTCACAGGACCCAAAGAGAGATGATGTGAAAAGAGAGATCCAGAGAA 201
QY 181 GAGGAAAGCATGGCAAGTGGGACGATGCGGCCGAAAGGAATTAAGAGAGAACTGGGT 240
DB 202 GAGGAAAGCATGGCAAGTGGGACGATGCGGCCGAAAGGAATTAAGAGAGAACTGGGT 261
QY 241 CATATGGGAGATCGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGAGGGTGCACAA 300
DB 262 CATATGGGAGATCAGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGAGGGTGCACAA 321
QY 301 GGGGAAAGGTTTGTGGAATACCTGGAGAAAGGCAAGCAAGCAGTACTGTCTGTAT 360
DB 322 GGGGAAAGGTTTGTGGAATACCTGGAGAAAGGCAAGCAAGCAGTACTGTCTGTAT 381
QY 361 TGTGGAAGATACCGGAAATTTGTTGGACAACTGGATATTAGTATTTCCCGGTCAAGACA 420
DB 382 TGTGGAAGATACCGGAAATTTGTTGGACAACTGGATATTAGTATTTCCCGGTCAAGACA 441
QY 421 TCTATGAAGTTTGTCAAGAAATGTGATAGAGGGATTAGGGAATCTGAAGAAATTTCTAC 480
DB 442 TCTATGAAGTTTGTCAAGAAATGTGATAGAGGGATTAGGGAATCTGAAGAAATTTCTAC 501
QY 481 TACATCGTGCAGGAAGAGAAACTACAGGGAATCCCTAACCCACTGCAGGATTCGGGT 540
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RESULT 9

US-09-978-403A-96
; Sequence 96 Application US/09978403A
; Publication No. US20030050240A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Flivaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
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; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C17
; CURRENT APPLICATION NUMBER: US/09/978,403A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 09/918585
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QY 181 GAGGAAAGCATGCGCAATGAGGAGATGAGGAGATGAGGAGATGAGGAGATGAGGAGAT 240
DB 202 GAGGAAAGCATGCGCAATGAGGAGATGAGGAGATGAGGAGATGAGGAGATGAGGAGAT 261
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DB 382 TGTGGAAGATACCGGAAATTTGTTGGACCACTGATATTAGTATTGCTCCCGCTCAAGACA 441
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DB 442 TCTATGAAGTTTGTCAAGAAATGTGATAGCAGGAGATTAGGAAACTGAAGAGAAATTTCTAC 501
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DB 562 GGAATGCTAGCCATGCCCCAAGGATGAAGCTGCCAAACACACTCATCTGCTGACTATGTTGCC 621
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DB 682 ATGTTTCAGAGACAACTCCACTGCGAGAACTATAGCAACTGGAATGAGGGGAAACCCAGC 741
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DB 742 GACCCCTATGCTATGAGGAGCTGTGAGAGATGCTGAGCTCTGGCAGATGGAATGACACA 801
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DB 802 GAGTGCCATCTTACCATGTTCTGTTGAGTTTCATCAAGAGAGAGAGAGAG 852

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RESULT 10
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; Sequence 96, Application US/09978564A
; Publication No. US20030050241A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavin, Ivar J.

```

APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Acids and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC25
CURRENT APPLICATION NUMBER: US/09/978,564A
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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Query Match 81.6%; Score 678; DB 10; Length 1016;
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DB 382 TGTGAAGATACCGGAATTTGTTGGCAACTGGATATTAGTATTCGCGGCTCAAGACA 441
QY 421 TCTATGAATTTGTCAAGATGTGATAGCAGGATAGGGAATCTGAAGAGAAATTTCTAC 480
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DB 802 GAGTGCCATCTTACCATGTACTTTGTCTGTGAGTTTCATCAAGAAGAAAAAG 852

RESULT 11
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; Sequence 96, Application US/09999833A
; Publication No. US20030054405A1
; GENERAL INFORMATION:
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; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
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; APPLICANT: Eaton, Dan
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; APPLICANT: Filvaroff, Ellen
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; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C65
; CURRENT APPLICATION NUMBER: US/09/999, 833A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
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; PRIOR APPLICATION NUMBER: 60/085697

Query Match      81.6%; Score 678; DB 10; Length 1016;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 61 TTGCAAAATTCAGAGTCTGGGTCTGATATTTAGTACCGCTCTACCGCTGAAGTCTGTGCC 120
Db 82 TTGCAAAATTCAGAGTCTGGGTCTGATATTTAGTACCGCTCTACCGCTGAAGTCTGTGCC 141
QY 121 ACACACACAATTTACCGAGACCCAAAGGAGATGATGTGTAAGAGGAGATCCAGAGAA 180
Db 142 ACACACACAATTTACCGAGACCCAAAGGAGATGATGTGTAAGAGGAGATCCAGAGAA 201
QY 181 GAGGGAAGCATGGCAAGTGGGAGCGCATGGGGCCGAAGGAATTAAGAGAACTGGGT 240
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QY 241 GATATGGGAGATCGGGGCAATATTCGCAAGACTGGGCCCATTTGGGAAGAGGGTGACAA 300
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QY 301 GGGGAAAAAGTTTGTCTGGATATCTGAGAAAAGCCAAAGCAGGTACTGTCTGTGAT 360
Db 322 GGGGAAAAAGTTTGTCTGGATATCTGAGAAAAGCCAAAGCAGGTACTGTCTGTGAT 381
QY 361 TGTGGAAGATACCGGAATTTCTTGCAACTTGGATATTTAGTATTCCTCCGCTCAAGACA 420
Db 382 TGTGGAAGATACCGGAATTTCTTGCAACTTGGATATTTAGTATTCCTCCGCTCAAGACA 441
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Db 442 TCTATGAAGTTTCTCAAGATGTAGTACGAGGATAGGGAATCTGAAGAGAAATTTCTAC 501
QY 481 TACATGTCGAGAGAGAGAACTACAGGATCCCTAACCCACTGCAGATTCGGGGT 540
Db 502 TACATGTCGAGAGAGAGAACTACAGGATCCCTAACCCACTGCAGATTCGGGGT 561
QY 541 GGAATCTAGCCATGCCCAAGGATGAAGTCCCAACACACTCATCGTGTGATTTGCC 600
Db 562 GGAATCTAGCCATGCCCAAGGATGAAGTCCCAACACACTCATCGTGTGATTTGCC 621
QY 601 AAGAGTGGCTTTCTTCGGGTGTTTATTCGGGTGAATGACCTTGAAGAGGAGGACAGTAC 660
Db 622 AAGAGTGGCTTTCTTCGGGTGTTTATTCGGGTGAATGACCTTGAAGAGGAGGACAGTAC 681
QY 661 ATGTTCCACAGACAACTCCACTGCAGAACTATAGCAACTGGAATAGGGGGAAACCCAGC 720
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QY 721 GACCCCTATGTCATGAGACTGTGTGAGATGCTGAGCTCTGCAGATGGAATGACACA 780
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QY 781 GAGTGCATCTTACCATGTACTTCTGTGAGTTTCATCAAGAGAAAG 831
Db 802 GAGTGCATCTTACCATGTACTTCTGTGAGTTTCATCAAGAGAAAG 852

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RESULT 12

US-09-981-915A-96
; Sequence 96, Application US/09981915A
; Publication No. US20030054986A1
; GENERAL INFORMATION:

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; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
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; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
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 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 81.6%; Score 678; DB 10; Length 1016;

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QY	61	TTGCAAAATTCAGATCTGGTCTCGATATTGATAGCGCTCTACCGCTGAAGTCTGTGC	120
DB	82	TTGCAAAATTCAGATCTGGTCTCGATATTGATAGCGCTCTACCGCTGAAGTCTGTGC	141
QY	121	ACACACACAATTTTCACAGGACCCAAAGGAGATGATGTTGAAAGGAGATCCAGAGAA	180
DB	142	ACACACACAATTTTCACAGGACCCAAAGGAGATGATGTTGAAAGGAGATCCAGAGAA	201
QY	181	GAGGAAAGCATGGCAAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	240
DB	202	GAGGAAAGCATGGCAAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	261
QY	241	GATATGGGAGATCGGGGCAATATTGGCAAGACTGGGCCCATATTGGGAGAGAGGCTGACAA	300

Db	262	GATATGGGAGATCAGGCAATATGGCAAGACTGGCCCATTTGGAGAGAGGTGACAA	321	TITLE OF INVENTION: Acids Encoding the Same
QY	301	GGGAAAAGGTTTGGTGGATACCTGGAGAAAAGCAAGCAAGTATGCTGTGTAT	360	FILE REFERENCE: P2630P1C14
Db	322	GGGAAAAGGTTTGGTGGATACCTGGAGAAAAGCAAGCAAGTATGCTGTGTAT	381	CURRENT APPLICATION NUMBER: US/09/978,824
QY	361	TGTGGAAGATACCGGAATTTGTTGGACAACTGGATATTAGTATGCTCCGGCTCAAGACA	420	PRIOR FILING DATE: 2001-10-17
Db	382	TGTGGAAGATACCGGAATTTGTTGGACAACTGGATATTAGTATGCTCCGGCTCAAGACA	441	PRIOR APPLICATION NUMBER: 09/918585
QY	421	TCTATGAAGTTGTCAAGATGTGTATGACAGGATTTAGGAAAAGTGAAGAAAATTTCTAC	480	PRIOR FILING DATE: 2001-07-30
Db	442	TCTATGAAGTTGTCAAGATGTGTATGACAGGATTTAGGAAAAGTGAAGAAAATTTCTAC	501	PRIOR FILING DATE: 2001-07-30
QY	481	TACATCGTGCAGAGAGAGAACTACAGGAACTCCCTAACCCACTGCAGGATTCGGGGT	540	PRIOR APPLICATION NUMBER: 60/062250
Db	502	TACATCGTGCAGAGAGAGAACTACAGGAACTCCCTAACCCACTGCAGGATTCGGGGT	561	PRIOR FILING DATE: 1997-10-17
QY	541	GGAACTGCTAGCCATCCCAAGATGAAGCTGCCAACACACTCATCGCTGACTATGTGCC	600	PRIOR APPLICATION NUMBER: 60/064249
Db	562	GGAACTGCTAGCCATCCCAAGATGAAGCTGCCAACACACTCATCGCTGACTATGTGCC	621	PRIOR FILING DATE: 1997-11-03
QY	601	AGAGTGGCTTCTTCGGGTGTTCAATGGCGTGAATGACCTTGAAGGGAGGACAGTAC	660	PRIOR APPLICATION NUMBER: 60/065311
Db	622	AGAGTGGCTTCTTCGGGTGTTCAATGGCGTGAATGACCTTGAAGGGAGGACAGTAC	681	PRIOR FILING DATE: 1997-11-13
QY	661	ATGTTTCACAGACAACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGAAACCCAGC	720	PRIOR APPLICATION NUMBER: 60/066364
Db	682	ATGTTTCACAGACAACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGAAACCCAGC	741	PRIOR FILING DATE: 1997-11-21
QY	721	GACCCCTATGTCATGAGCACTGTGTGAGATGCTGAGCTCTGCGACATGGATGACACA	780	PRIOR APPLICATION NUMBER: 60/077450
Db	742	GACCCCTATGTCATGAGCACTGTGTGAGATGCTGAGCTCTGCGACATGGATGACACA	801	PRIOR FILING DATE: 1998-03-10
QY	781	GAGTGCCTATTTACCATGCTACTTGTCTGTGAGTTCATCAAGAGAAAAAG	831	PRIOR APPLICATION NUMBER: 60/077632
Db	802	GAGTGCCTATTTACCATGCTACTTGTCTGTGAGTTCATCAAGAGAAAAAG	852	PRIOR FILING DATE: 1998-03-11
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US-09-978-824-96				PRIOR FILING DATE: 1998-03-12
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GENERAL INFORMATION:				PRIOR APPLICATION NUMBER: 60/078886
APPLICANT: Ashkenazi, Avi				PRIOR FILING DATE: 1998-03-20
APPLICANT: Baker Kevin P.				PRIOR APPLICATION NUMBER: 60/078936
APPLICANT: Botstein, David				PRIOR FILING DATE: 1998-03-20
APPLICANT: Desnoyers, Luc				PRIOR APPLICATION NUMBER: 60/078910
APPLICANT: Eaton, Dan				PRIOR FILING DATE: 1998-03-20
APPLICANT: Ferrara, Napoleon				PRIOR APPLICATION NUMBER: 60/078939
APPLICANT: Fong, Sherman				PRIOR FILING DATE: 1998-03-25
APPLICANT: Gao, Wei-Qiang				PRIOR APPLICATION NUMBER: 60/079656
APPLICANT: Gerber, Hanspeter				PRIOR FILING DATE: 1998-03-26
APPLICANT: Gerritsen, Mary E.				PRIOR APPLICATION NUMBER: 60/079689
APPLICANT: Goddard, Audrey				PRIOR FILING DATE: 1998-03-27
APPLICANT: Godowski, Paul J.				PRIOR APPLICATION NUMBER: 60/079663
APPLICANT: Grimaldi, J. Christopher				PRIOR FILING DATE: 1998-03-27
APPLICANT: Gurney, Austin L.				PRIOR APPLICATION NUMBER: 60/079728
APPLICANT: Hillan, Kenneth J.				PRIOR FILING DATE: 1998-03-27
APPLICANT: Kljavin, Ivar J.				PRIOR APPLICATION NUMBER: 60/079786
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APPLICANT: Napier, Mary A.				PRIOR APPLICATION NUMBER: 60/079920
APPLICANT: Pan, James				PRIOR FILING DATE: 1998-03-30
APPLICANT: Paoni, Nicholas F.				PRIOR APPLICATION NUMBER: 60/079923
APPLICANT: Roy, Margaret Ann				PRIOR FILING DATE: 1998-03-30
APPLICANT: Shelton, David L.				PRIOR APPLICATION NUMBER: 60/080105
APPLICANT: Stewart, Timothy A.				PRIOR FILING DATE: 1998-03-31
APPLICANT: Tumas, Daniel				PRIOR APPLICATION NUMBER: 60/080107
APPLICANT: Williams, P. Mickey				PRIOR FILING DATE: 1998-03-31
APPLICANT: Wood, William I.				PRIOR APPLICATION NUMBER: 60/080165
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic				PRIOR FILING DATE: 1998-03-31
				PRIOR APPLICATION NUMBER: 60/080194
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Best Local Similarity 99.6%; Pred. No. 0;
Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ATGAATGGCTTTGTCATCCTTTGCTTTCGAAGAAACCAATTTATCCTCTGTGACTATTCTT 60
Db 22 ATGAATGGCTTTGTCATCCTTTGCTTTCGAAGAAACCAATTTATCCTCTGTGACTATTCTT 81
QY 61 TTGCAATTCAGAGTCGGGTCTGGATTTGATAGCGGCTTACCGCTGAAGTCTGTGCC 120
Db 82 TTGCAATTCAGAGTCGGGTCTGGATTTGATAGCGGCTTACCGCTGAAGTCTGTGCC 141
QY 121 ACACACACAATTTCCACCAGGACCCAAAGAGAGATGATGGTGAAGAAAGAGATCCAGAGAA 180
Db 142 ACACACACAATTTCCACCAGGACCCAAAGAGAGATGATGGTGAAGAAAGAGATCCAGAGAA 201
QY 181 GAGGAAAGCATGCAAAAGTGGGACCGATGGGCGGCAAGAGGATTAAGAGAGAACTGGGT 240
Db 202 GAGGAAAGCATGCAAAAGTGGGACCGATGGGCGGCAAGAGGATTAAGAGAGAACTGGGT 261
QY 241 GATATGGGAGATCGGGCAATTTGGCAAGACTGGGCCCATTTGGGAGAGAGGATGACAAA 300
Db 262 GATATGGGAGATCAGGGCAATTTGGCAAGACTGGGCCCATTTGGGAGAGAGGATGACAAA 321
QY 301 GGGGAAAAAGGTTTGGTGGATACCTGGAGAAAAAGGCAAGCAGGACTGTCTGTGAT 360
Db 322 GGGGAAAAAGGTTTGGTGGATACCTGGAGAAAAAGGCAAGCAGGACTGTCTGTGAT 381
QY 361 TGTGGAAGATACCGGAAATTTGTTGGACAACTGGATATTAGTATTGCCCGGCTCAAGACA 420
Db 382 TGTGGAAGATACCGGAAATTTGTTGGACAACTGGATATTAGTATTGCCCGGCTCAAGACA 441
QY 421 TCTATGAAGTTTGTCAAGATGTGATAGCGGATTTAGGGAATCTGAAGAGAAATCTTAC 480
Db 442 TCTATGAAGTTTGTCAAGATGTGATAGCGGATTTAGGGAATCTGAAGAGAAATCTTAC 501
QY 481 TACATCGTGCAGGAGAGAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGGGGT 540
Db 502 TACATCGTGCAGGAGAGAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGGGGT 561
QY 541 GGAATGCTAGCCATGCCCAAGGATGAAGTGCAGCAACACATCATTCGTGTGATGTGTGCC 600
Db 562 GGAATGCTAGCCATGCCCAAGGATGAAGTGCAGCAACACATCATTCGTGTGATGTGTGCC 621
QY 601 AAGAGTGGCTTCTTTCGGGTGTTTCATTGGGTGATGACCTTGAAGGGAGGACAGTAC 660
Db 622 AAGAGTGGCTTCTTTCGGGTGTTTCATTGGGTGATGACCTTGAAGGGAGGACAGTAC 681
QY 661 ATGTTTCACAGACAACACTCCACTCCAGAACTATAGCAACTGGAATGAGGGGGAACCCAGC 720

Query Match 81.6%; Score 678; DB 10; Length 1016;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 82 TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCGCTCTTACCGCTGAAGTCTGTGCC 141
QY 121 ACACACCAATTTCCAGACCCCAAGGAGATGATGGTGAAGAGGAGATCCAGAGAA 180
DB 142 ACACACCAATTTCCAGACCCCAAGGAGATGATGGTGAAGAGGAGATCCAGAGAA 201
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DB 202 GAGGAAAGCATGGCAAGTGGGACGATGGGCGCCGAAAGGAATTAAGAGAGAACTGGGT 261
QY 241 CATATGGGAGATCGGGCAATATTGGCAAGACTGGGCGCCCATTTGGGAAGAGGGTGACAA 300
DB 262 CATATGGGAGATCAGGGCAATATTGGCAAGACTGGGCGCCCATTTGGGAAGAGGGTGACAA 321
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DB 322 GGGGAAAGGTTTGGCTTGGAAATCTGAGAGAAAGGCAAGCAGGTACTGTCTGTAT 381
QY 361 TGTGAAAGATACCGGAAATTTGTTGGCAAACTGGATATTAGTATTGCCGGCTCAAGACA 420
DB 382 TGTGAAAGATACCGGAAATTTGTTGGCAAACTGGATATTAGTATTGCCGGCTCAAGACA 441
QY 421 TCTATGAAGTTTGTCAAGAAATGTCATAGCAGGATAGGGAAGAACTGAAGAGAAATTTCTAC 480
DB 442 TCTATGAAGTTTGTCAAGAAATGTCATAGCAGGATAGGGAAGAACTGAAGAGAAATTTCTAC 501
QY 481 TACATCGTGCAGGAGAGAAACTACAGGAAATCCCTAACCCACTGCAGGATTCGGGT 540
DB 502 TACATCGTGCAGGAGAGAAACTACAGGAAATCCCTAACCCACTGCAGGATTCGGGT 561
QY 541 GGAATGCTAGCCATGCCPAGGATGAGCTGCCAACAACACTCATCTGCTGCTATGTTGCC 600
DB 562 GGAATGCTAGCCATGCCPAGGATGAGCTGCCAACAACACTCATCTGCTGCTATGTTGCC 621
QY 601 AAGAGTGGCTTTCTTTTCGGGTGTTTCATTGGCGTGAATGACCTTGAAGAGGAGGACAGTAC 660
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QY 661 ATGTTCAAGACAACTCCACTGCAGAACTATAGCACTGGATGAGGGGAAACCCAGC 720
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DB 802 GAGTGGCAATCTTACCATGTTCTTTGTTGTGTGAGTTCTATCAGNAGAGAAAAG 852

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; Publication No. US20030069178A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Borstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Forgi, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
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FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PLC21
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;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 81.6%; Score 678; DB 10; Length 1016;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 ATGAATGGCTTTGGCATCTCTTTCGAAGAAACCAATTTATCCTCTCGGTACTATTTCCT 60
Db |||||
Qy 22 ATGAATGGCTTTGGCATCTCTTTCGAAGAAACCAATTTATCCTCTCGGTACTATTTCCT 81
Db |||||
Qy 61 TTGCAAAATTCAGAGTCTGGTCTGGATATTGATAGCGGTCTTACCGCTGAAGTCTGTGCC 120
Db |||||
Qy 82 TTGCAAAATTCAGAGTCTGGTCTGGATATTGATAGCGGTCTTACCGCTGAAGTCTGTGCC 141
Db |||||
Qy 121 ACACACAAATTTCCAGGACCCAAAAGGAGATGATGGTAAAAGGAGATCCAGGAGAA 180
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Qy 142 ACACACAAATTTCCAGGACCCAAAAGGAGATGATGGTAAAAGGAGATCCAGGAGAA 201
Db |||||
Qy 181 GAGGGAAGCATGGCAAGTGGGACGCTGGGCGGAAGGAATTAAGGAGAACTGGGT 240
Db |||||
Qy 202 GAGGGAAGCATGGCAAGTGGGACGCTGGGCGGAAGGAATTAAGGAGAACTGGGT 261
Db |||||
Qy 241 GATATGGGAGATCGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGAGGGTGACAAA 300
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Qy 382 TGTGGAAGATACCGGAAATTTGTTGCAACCTGGATATTAGTATTCGCCGCTCAAGACA 441
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Qy 421 TCTATGAAGTTTGTCTCAGANTGTGATAGCAGGGATTAGGGAACCTGAAGGAAATTTCTAC 480
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Qy 442 TCTATGAAGTTTGTCTCAGANTGTGATAGCAGGGATTAGGGAACCTGAAGGAAATTTCTAC 501
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Qy 802 GAGTGCCATCTTACCATGTACTTTGTGTGAGTTTCATCAAGAGAGAAAAG 852
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Search completed: March 11, 2004, 20:36:29
Job time : 365 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 18:36:34 ; Search time 2526 Seconds
(without alignments)
9824.019 Million cell updates/sec

Title: US-09-600-932-1_COPY_6_836

Perfect score: 831

Sequence: 1 atgaatgcttgcctcctt.....agttcatcaagaagaaag 831

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

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3: em_estim.*

4: em_estmu.*

5: em_estov.*

6: em_estpl.*

7: em_estro.*

8: em_htc.*

9: gb_est1.*

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19: em_gss_pln.*

20: em_gss_vrt.*

21: em_gss_fun.*

22: em_gss_mam.*

23: em_gss_mus.*

24: em_gss_pro.*

25: em_gss_rod.*

26: em_gss_phg.*

27: em_gss_vrl.*

28: gb_gss1.*

29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	729	✓ 87.7	834	29	AY409410 Homo sapi
2	608	73.2	834	29	AY409411 Pan trogl
3	523	62.9	752	12	EM009998 603630745
4	401	48.3	609	12	EM010788 603629302

5	364	43.8	560	13	BX494095
6	356	42.8	457	13	BX496500
7	228	27.4	747	14	CB228545
8	153	18.4	1239	12	BM551435
9	148	17.8	326	14	R29493
10	148	17.8	670	14	CB141360
11	138	16.6	735	13	BM090456
12	116	14.0	362	14	R97480
13	75	9.0	354	10	AM435866
14	75	9.0	492	10	BF078010
15	72	8.7	357	9	AV653117
16	71	8.5	499	12	BI467460
17	48	5.8	368	14	W00944
18	29	3.5	636	13	BM671934
19	29	3.5	783	29	CC909869
20	28	3.4	834	29	AY409412
21	28	3.4	955	10	BB612129
22	28	3.4	4591	11	AK028423
23	26	3.1	324	13	BY331120
24	26	3.1	325	13	BY332718
25	26	3.1	361	10	BB869996
26	26	3.1	701	29	CE765022
27	23	2.8	344	13	BY008444
28	23	2.8	380	10	BB869893
29	23	2.6	613	13	CA052606
30	22	2.6	246	10	BF881627
31	22	2.6	553	14	CA817970
32	22	2.6	703	14	CB467812
33	22	2.6	823	14	CK147387
34	21	2.5	473	12	BM571216
35	21	2.5	486	12	BM426695
36	21	2.5	515	28	AQ972105
37	21	2.5	529	12	BM571381
38	21	2.5	590	9	AV699021
39	21	2.5	654	12	BI067078
40	21	2.5	780	28	BZ198292
41	21	2.5	872	14	CD755784
42	21	2.5	1000	29	ECA576754
43	20	2.4	121	10	BF020755
44	20	2.4	170	9	AW051664
45	20	2.4	231	10	BB078045

ALIGNMENTS

RESULT 1
AY409410
LOCUS
DEFINITION
Homo sapiens COLEC10 gene, VIRTUAL TRANSCRIPT, partial sequence,
Genomic survey sequence.
ACCESSION
AY409410
VERSION
AY409410.1
KEYWORDS
GSS.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 834)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL
Science 302 (5652), 1960-1963 (2003)
PUBMED
14671302
REFERENCE
2 (bases 1 to 834)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE
Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES
source Location/Qualifiers
1..834
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
<1..>834
gene /gene="COLEC10"
/locus_tag="HCM3548"
ORIGIN
Query Match 87.7%; Score 729; DB 29; Length 834;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 829; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 ATGAATGGCTTTGCATCCCTTGGTTCGAAGAACCATTATTCCTCTGGTACTATTCTT 60
Db 1 ATGAATGGCTTTGCATCCCTTGGTTCGAAGAACCATTATTCCTCTGGTACTATTCTT 60
Qy 61 TTGCAAAATTCAGAGTCTGGTCTGGATATTGATAGCCGCTCTACCGCTGAAGTCTGTGCC 120
Db 61 TTGCAAAATTCAGAGTCTGGTCTGGATATTGATAGCCGCTCTACCGCTGAAGTCTGTGCC 120
Qy 121 ACACACACAAATTCACAGACCCCAAGAGATGATGTTGAAGAAGAGATCCAGAGAA 180
Db 121 ACACACACAAATTCACAGACCCCAAGAGATGATGTTGAAGAAGAGATCCAGAGAA 180
Qy 181 GAGGAAAGCATGGCAAGTGGGACGATGGGGCGGAAAGGAATTAAGAGAGAACTGGGT 240
Db 181 GAGGAAAGCATGGCAAGTGGGACGATGGGGCGGAAAGGAATTAAGAGAGAACTGGGT 240
Qy 241 GATATGGAGATCGGGCAATATTGGCAAGACTGGGCCCATTTGGAGAGAGGGTGACAAA 300
Db 241 GATATGGAGATCGGGCAATATTGGCAAGACTGGGGCCCATTTGGAGAGAGGGTGACAAA 300
Qy 301 GGGGAAAAAGGTTTGTCTGGAATACCTGGAGAAAAGCAAGCAGGTACTGTCTGTGAT 360
Db 301 GGGGAAAAAGGTTTGTCTGGAATACCTGGAGAAAAGCAAGCAGGTACTGTCTGTGAT 360
Qy 361 TGTGGAAGATACCGGAAATTTGTGGACAACTGGATATTAGTATGTCCTCGGCTCAAGACA 420
Db 361 TGTGGAAGATACCGGAAATTTGTGGACAACTGGATATTAGTATGTCCTCGGCTCAAGACA 420
Qy 421 TCTATCAAGTTTGTCAAGATGTGATAGCAGGATTTAGGGAATCTGAAGAGAAATCTTAC 480
Db 421 TCTATCAAGTTTGTCAAGATGTGATAGCAGGATTTAGGGAATCTGAAGAGAAATCTTAC 480
Qy 481 TACATCGTGAAGAGAGAACTACAGGGAATCCCTTAACCCACTGACAGATTCGGGGT 540
Db 481 TACATCGTGAAGAGAGAACTACAGGGAATCCCTTAACCCACTGACAGATTCGGGGT 540
Qy 541 GGAATCTAGCATGCCCCAAGATGAGCTGCAACACACTCATCGCTGACTATGTTGCC 600
Db 541 GGAATCTAGCATGCCCCAAGATGAGCTGCAACACACTCATCGCTGACTATGTTGCC 600
Qy 601 AAGAGTGGCTTCTTTCCGGTGTTCATTTGGCGTGAATACCTTGAAGAGGGGACAGTAC 660
Db 601 AAGAGTGGCTTCTTTCCGGTGTTCATTTGGCGTGAATACCTTGAAGAGGGGACAGTAC 660
Qy 661 ATGTTTCACAGACAACTCCATCGAGAACTATAGCAATCTGAAATGAGGGGAAACCCAGC 720
Db 661 ATGTTTCACAGACAACTCCATCGAGAACTATAGCAATCTGAAATGAGGGGAAACCCAGC 720
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Db 721 GACCCCTATGTTTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACA 780
Qy 781 GAGTGCATCTACCATGACTTCTGTGTGATGTTTCATCAGAGAGAAAG 831
Db 781 GAGTGCATCTACCATGACTTCTGTGTGATGTTTCATCAGAGAGAAAG 831

RESULT 2
LOCUS AY409411 834 bp DNA linear GSS 16-DEC-2003
DEFINITION Pan troglodytes COLEC10 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY409411
VERSION AY409411.1 GI:39765379
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE 1 (bases 1 to 834)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 834)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES
source Location/Qualifiers
1..834
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1..>834
/gene="COLEC10"
/locus_tag="HCM3548"
ORIGIN
Query Match 73.2%; Score 608; DB 29; Length 834;
Best Local Similarity 99.5%; Pred. No. 2;le-288;
Matches 808; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 20 TGCTTCGAAGAAACCAATTATCTCTCTGCTGCTATTTCTTTTGCATAATTCAGAGTCTGG 79
Db 20 TGCTTCGAAGAAACCAATTATCTCTCTGCTGCTATTTCTTTTGCATAATTCAGAGTCTGG 79
Qy 80 GTCTGGATATTGATAGCGCTCTACCGCTGAAGTCTGTGCCACACACACATTTCCACCAG 139
Db 80 GTCTGGATATTGATAGCGCTCTACCGCTGAAGTCTGTGCCACACACACATTTCCACCAG 139
Qy 140 GACCCAAAGGAGATGATGTTGAAGAAGAGATCCAGGAGAGAGGAGGAGCATGGCAAG 199
Db 140 GACCCAAAGGAGATGATGTTGAAGAAGAGATCCAGGAGAGAGGAGGAGCATGGCAAG 199
Qy 200 TGGGACCATCGGGCCGAAAGGAATTAAGAGAGAACTGGGTGATATGGGAGATCGGGGCA 259
Db 200 TGGGACCATCGGGCCGAAAGGAATTAAGAGAGAACTGGGTGATATGGGAGATCGGGGCA 259
Qy 260 ATATTGGCAAGACTGGGCCCATTTGGGAAGAGGTGACAAAGGGGAAAAAGGTTTGCCTTG 319
Db 260 ATATTGGCAAGACTGGGCCCATTTGGGAAGAGGTGACAAAGGGGAAAAAGGTTTGCCTTG 319
Qy 320 GAATACCTGGAGAAAAAGGCAAGCAGGTACTGTCTGTGATTTGTGAAGATACCGGAAAT 379
Db 320 GCATACCTGGAGAAAAAGGCAAGCAGGTACTGTCTGTGATTTGTGAAGATACCGGAAAT 379
Qy 380 TTGTTGGCAACTGGATATTAGTATTGCCCGCTCAGACATCTATGAAGTTTGTCAAGA 439
Db 380 TTGTTGGCAACTGGATATTAGTATTGCCCGCTCAGACATCTATGAAGTTTGTCAAGA 439

Db 380 TTGTTGGACAACTGGATATTAGTATGCTCGCTCAGACATCTATGAAGTTTCTCAAGA 439
Qy 440 ATGTGATAGCAGGATAGGAAATGAAGAAATCTACTATACATCGTCAGGAAGAGA 499
Db 440 ATGTGATAGCAGGATAGGAAATCTAGGAATCTAGGAATCTACTATACATCGTCAGGAAGAGA 499
Qy 500 AGAATCTACAGGAAATCCCTAACCCACTCAGGATTCGGGTGGATCTAGCCATGCCCA 559
Db 500 AGAATCTACAGGAAATCCCTAACCCACTCAGGATTCGGGTGGATCTAGCCATGCCCA 559
Qy 560 AGGATGAAGTCCCAACACACTCATCGCTGACTATGTTGCCAAGAGTGGCTTCTTTTCGGG 619
Db 560 AGGATGAAGTCCCAACACACTCATCGCTGACTATGTTGCCAAGAGTGGCTTCTTTTCGGG 619
Qy 620 TGTTCATTGCGCTGAATGACCTTGAAGAGGAGGACAGTATCATGTTTTCACAGACACACTC 679
Db 620 TGTTCATTGCGCTGAATGACCTTGAAGAGGAGGACAGTATCATGTTTTCACAGACACACTC 679
Qy 680 CACTGCAGAACTATAGCAACTGGAATGAGGGGGAAACCCAGCAGCCCTATGCTCATGAGG 739
Db 680 CACTGCAGAACTATAGCAACTGGAATGAGGGGGAAACCCAGCAGCCCTATGCTCATGAGG 739
Qy 740 ACTGTGTGAGATGCTGAGCTCTGCAGATGGAATGACAGAGTGCCATCTTACCATGT 799
Db 740 ACTGTGTGAGATGCTGAGCTCTGCAGATGGAATGACAGAGTGCCATCTTACCATGT 799
Qy 800 ACTTTGCTGTGAGTTTCATCAAGAGAAAGAAAG 831
Db 800 ACTTTGCTGTGAGTTTCATCAAGAGAAAGAAAG 831

RESULT 3
BM009998
LOCUS 603630745F1 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:544459 5',
DEFINITION mRNA sequence.
ACCESSION BM009998
VERSION BM009998.1 GI:16524352
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 752)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DFP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCW1923 row: j column: 12
High quality sequence stop: 752.
Location/Qualifiers
1..752
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:544459"
/tissue_type="amelanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="NIH MGC 41"
/clone_lib="NIH MGC 41"
/note="organ: skin; Vector: pOT7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and

Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN
Query Match 62.9%; Score 523; DB 12; Length 752;
Best Local Similarity 99.7%; Pred. No. 1.7e-246;
Matches 623; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 149 GAGATGATGTTGAAAAAGAGATCCAGGAGAAAGGAAAGCATGGCAAGTGGGACGCA 208
Db 6 GAGATGATGTTGAAAAAGAGATCCAGGAGAAAGGAAAGCATGGCAAGTGGGACGCA 65
Qy 209 TGGGCCCGAAAGGAATTAAGGAGAACTGGTGATATGGGAGATCGGGCAATATTGGCA 268
Db 66 TGGGCCCGAAAGGAATTAAGGAGAACTGGTGATATGGGAGATCAGGCAATATTGGCA 125
Qy 269 AGACTGGGCCCATTTGGGAAGAGGGTGACAAAGGGGAAAAAGGTTTCTTGGAAATACCTG 328
Db 126 AGACTGGGCCCATTTGGGAAGAGGGTGACAAAGGGGAAAAAGGTTTCTTGGAAATACCTG 185
Qy 329 GAGAAAGGCGAAAGCAGTACTCTCTGCTGATTTGTTGGAGATACCGGAATTTGTTGGAC 388
Db 186 GAGAAAGGCGAAAGCAGTACTCTCTGCTGATTTGTTGGAGATACCGGAATTTGTTGGAC 245
Qy 389 AACTGGATATTAGTATTGCTCCCGCTCAAGACATCTATGAAGTTTGTCAAGATGTGATAG 448
Db 246 AACTGGATATTAGTATTGCTCCCGCTCAAGACATCTATGAAGTTTGTCAAGATGTGATAG 305
Qy 449 CAGGATTAGGAACTGAAGAGAAATCTACTACATCTGTCAGGAGAGAGAGAACTACA 508
Db 306 CAGGATTAGGAACTGAAGAGAAATCTACTACATCTGTCAGGAGAGAGAGAACTACA 365
Qy 509 GGGATCCCTAACCCACTGCAGGATTCGGGGTGGAAATGCTTAGCCATGCCCAAGGATGAAG 568
Db 366 GGGATCCCTAACCCACTGCAGGATTCGGGGTGGAAATGCTTAGCCATGCCCAAGGATGAAG 425
Qy 569 CTGCCAACAACACTCATCGCTGACTATGTTGCTGCAAGAGTGGCTTCTTTGGGTGTTCAATG 628
Db 426 CTGCCAACAACACTCATCGCTGACTATGTTGCTGCAAGAGTGGCTTCTTTGGGTGTTCAATG 485
Qy 629 GCGTGAATGACTTTGAAGGAGGAGGACAGTACATGTTTCAAGACACACTCCACTGCAGA 688
Db 486 GCGTGAATGACTTTGAAGGAGGAGGACAGTACATGTTTCAAGACACACTCCACTGCAGA 545
Qy 689 ACTATAGCAACTGGATGAGGGGAAACCCAGCGACCCCTATGTCATAGGAGTGTGTGG 748
Db 546 ACTATAGCAACTGGATGAGGGGAAACCCAGCGACCCCTATGTCATAGGAGTGTGTGG 605
Qy 749 AGATGCTGAGCTCTGCGAGATGGAA 773
Db 606 AGATGCTGAGCTCTGCGAGATGGAA 630

RESULT 4
BM010788
LOCUS 603629302F1 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5434680 5',
DEFINITION mRNA sequence.
ACCESSION BM010788
VERSION BM010788.1 GI:16525142
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 609)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DFP
cDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: InCyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1CM912 row: c column: 01
High quality sequence stop: 608.
Location/Qualifiers

FEATURES

source
1. .609
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:543460"
/tissue_type="amelanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 41"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following s' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN

Query Match 48.3%; Score 401; DB 12; Length 609;
Best Local Similarity 100.0%; Pred. No. 2.4e-186; Indels 0; Gaps 0;
Matches 401; Conservative 0; Mismatches 0;
QY 431 TTGTCAAGATGTGATGACGAGGATTAGGAACTGGAAGAGAAATTTCTACTACATCGTGC 490
DB 69 TTGTCAAGATGTGATGACGAGGATTAGGAACTGGAAGAGAAATTTCTACTACATCGTGC 128
QY 491 AGAAGAAGAACTACAGGAAATCCCTAACCCACTGACGAGATTCGGGTGGAAATGCTAG 550
DB 129 AGAAGAAGAACTACAGGAAATCCCTAACCCACTGACGAGATTCGGGTGGAAATGCTAG 188
QY 551 CCATGCCCAAGATGAAGTGCACACACTCATCGCTGACTATGTTGCCAAGAGTGGCT 610
DB 189 CCATGCCCAAGATGAAGTGCACACACTCATCGCTGACTATGTTGCCAAGAGTGGCT 248
QY 611 TCCTTCGGGTGTTCAATGCGGTGAATGACCTTGAAGGGAGGACAGTACATGTTTCAG 670
DB 249 TCCTTCGGGTGTTCAATGCGGTGAATGACCTTGAAGGGAGGACAGTACATGTTTCAG 308
QY 671 ACAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGACCCAGGACCCCTATG 730
DB 309 ACAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGACCCAGGACCCCTATG 368
QY 731 GTCATGAGAACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACAGAGTGCATC 790
DB 369 GTCATGAGAACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACAGAGTGCATC 428
QY 791 TTACCATGTTACTTTGTCTGTGAGTTTCATCAAGAGAAAG 831
DB 429 TTACCATGTTACTTTGTCTGTGAGTTTCATCAAGAGAAAG 469

RESULT 5
BX494095 560 bp mRNA linear EST 04-SEP-2003
LOCUS
DEFINITION
DXFZp779A1511 r1 779 (synonym: hnccl) Homo sapiens cDNA clone
BX494095 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 560)

Wambutt,R., Heubner,D., Mewes,H.W., Weil,B., Amid,C., Oeanger,A.,

TITLE

JOURNAL

COMMENT

Fobo,G., Han,M. and Wiemann,S.
EST (Wambutt,R., Heubner,D., Mewes,H.W., Weil,B., Amid,C., et al.)
Unpublished (2003)
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Cloned from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
consortium of the German Genome Project.
No s1 sequence available.
This clone (DKFZp779A1511) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, Germany; Email: clone@rzd.de.

FEATURES

Location/Qualifiers
1. .560
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp779A1511"
/tissue_type="liver"
/dev_stage="fetal"
/lab_host="DH10B"
/clone_lib="779 (synonym: hnccl)"
/note="Vector: pSport1_Sfi; Site 1: SfiIA; Site 2: SfiIB"

ORIGIN

Query Match 43.8%; Score 364; DB 13; Length 560;
Best Local Similarity 99.6%; Pred. No. 4.2e-168; Indels 0; Gaps 0;
Matches 464; Conservative 0; Mismatches 2;
QY 1 ATGAATGCTTTGATCCTCTGCTTCGAAGAAACCAATTTATCTCTCTGCTACTATTTCCT 60
DB 95 ATGAATGCTTTGATCCTCTGCTTCGAAGAAACCAATTTATCTCTCTGCTACTATTTCCT 154
QY 61 TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCGCTCCTACCGCTGAAGTCTGTGC 120
DB 155 TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCGCTCCTACCGCTGAAGTCTGTGC 214
QY 121 ACACACACAAATTTCCACAGGACCCCAAGAGAGATGATGTTGAAAGAGAGATCCAGAGAA 180
DB 215 ACACACACAAATTTCCACAGGACCCCAAGAGAGATGATGTTGAAAGAGAGATCCAGAGAA 274
QY 181 GAGGAAAGCATGCGAAAGTGGGACCGATGCGGCGGAAGAGATTAAGAGAGACTGGGT 240
DB 275 GAGGAAAGCATGCGAAAGTGGGACCGATGCGGCGGAAGAGATTAAGAGAGACTGGGT 334
QY 241 GATATGGGAGATCGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGAGAGGTGACAA 300
DB 335 GATATGGGAGATCGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGAGAGGTGACAA 394
QY 301 GGGGAAAAAGTTTGTCTTGGAAATACCTGGAGAAAAAGGCAAGCAGGTACTGTCTGTGAT 360
DB 395 GGGGAAAAAGTTTGTCTTGGAAATACCTGGAGAAAAAGGCAAGCAGGTACTGTCTGTGAT 454
QY 361 TGTGGAAGATACCGGAAATTTGTTGGCAACTGATATTAGTATTGCCCGGCTCAAGACA 420
DB 455 TGTGGAAGATACCGGAAATTTGTTGGCAACTGATATTAGTATTGCCCGGCTCAAGACA 514
QY 421 TCTATGAAGTTTGTCAAGAAATGTCATACGAGGATAGGGAAGCTG 466
DB 515 TCTATGAAGTTTGTCAAGAAATGTCATACGAGGATAGGGAAGCTG 560

RESULT 6

BX496500

LOCUS

DEFINITION

DXFZp779M0527 r1 779 (synonym: hnccl) Homo sapiens cDNA clone

BX496500 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 457)
AUTHORS Koehrer, K., Beyer, A., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S.
TITLE EST (Koehrer, K., Beyer, A., Mewes, H.W., Weil, B., Amid, C., et al.)
JOURNAL Unpublished (2003)
COMMENT Contact: MIPS
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
Heine-University, Dueseldorf/Germany) within the cDNA sequencing consortium of the German Genome Project. No sl sequence available.
This clone (DKFZp79M0527) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
1. 457
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp79M0527"
/tissue type="liver"
/dev stage="fetal"
/lab host="DH10B"
/clone lib="779 (synonym: hnccl)"
/note="Vector: pSPORT1_Sfi; Site_1: SfiIA; Site_2: SfiIB"
ORIGIN
Query Match 42.8%; Score 356; DB 13; Length 457;
Best Local Similarity 99.8%; Pred. No. 3.6e-164;
Matches 406; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGAATGCTTGCATCTCTTCGAGAAACCAATTTATCTCTCTGCTACTATTTCTT 60
DB 27 ATGAATGCTTGCATCTCTTCGAGAAACCAATTTATCTCTCTGCTACTATTTCTT 86
QY 61 TTGCAAAATTCAGAGTCTGGGTCTGGATATGATAGCGCTCTACCGCTGAAGTCTGTGCC 120
DB 87 TTGCAAAATTCAGAGTCTGGGTCTGGATATGATAGCGCTCTACCGCTGAAGTCTGTGCC 146
QY 121 ACACACAAATTCACAGGACCCAAAGGAGATGATGGTGAAGAAAGAGATCCAGAGAA 180
DB 147 ACACACAAATTCACAGGACCCAAAGGAGATGATGGTGAAGAAAGAGATCCAGAGAA 206
QY 181 GAGGAAAGAGATGCGCAAGTGGGACGATGGGCGGCAAGAGAAATTAAGGAGAACTGGGT 240
DB 207 GAGGAAAGAGATGCGCAAGTGGGACGATGGGCGGCAAGAGAAATTAAGGAGAACTGGGT 266
QY 241 GATATGGAGATCGGGGCAATATTGGCAAGCTGGGCCCATTTGGGAAGAGAGGTGACAA 300
DB 267 GATATGGAGATCGGGGCAATATTGGCAAGCTGGGCCCATTTGGGAAGAGAGGTGACAA 326
QY 301 GGGGAAAGAGTCTGTTGGATACCTGGGAGAAAGGCAAGCAGTACTCTGTGAT 360
DB 327 GGGGAAAGAGTCTGTTGGATACCTGGGAGAAAGGCAAGCAGTACTCTGTGAT 386
QY 361 TGTGGAAGATCCGGAAATTTGTTGGACAACTGGATATTAGTATTC 407
DB 387 TGTGGAAGATCCGGAAATTTGTTGGACAACTGGATATTAGTATTC 433
RESULT 7
CB228545
LOCUS
DEFINITION AGNCOURT 11505973 NICHD Rh_Ov1 Macaca mulatta cDNA clone
IMAGE:6886251 5', mRNA sequence.
ACCESSION CB228545

CB228545.1 GI:28280123
EST.
Macaca mulatta (rhesus monkey)
Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae; Cercopithecinae; Macaca.
1 (bases 1 to 747)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps@mail.nih.gov
Tissue Procurement: Dr. Eliot Spindel
cDNA Library Preparation: CLONTECH
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM3139 row: a column: 02
High quality sequence stop: 526.
Location/Qualifiers
1. 747
/organism="Macaca mulatta"
/mol_type="mRNA"
/db_xref="taxon:9544"
/clone="IMAGE:6886251"
/tissue type="Ovary"
/lab host="DH10B (phage-resistant)"
/clone lib="NICHD Rh_Ov1"
/note="Organ: ovary; Vector: pDNR-LIB; Site_1: Sfi I; Site_2: Sfi I; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.0-4.0 kb. Tissue pooled from pre-pubertal, post pubertal and menopausal monkeys. Constructed by Clontech. Note: this is a NICHD Library."
ORIGIN
Query Match 27.4%; Score 228; DB 14; Length 747;
Best Local Similarity 99.4%; Pred. No. 5e-101;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 436 AAGAATGTATACAGGATAGGAACTGAGAGAACTGAGAGAACTTACTATGCTGAGAA 495
DB 3 AAGAATGTATACAGGATAGGAACTGAGAGAACTGAGAGAACTTACTATGCTGAGAA 62
QY 496 GAGAAGAACTACAGGAACTCCCTTAACCCACTGAGGATTCGGGGTGAATGCTAGCCATG 555
DB 63 GAGAAGAACTACAGGAACTCCCTTAACCCACTGAGGATTCGGGGTGAATGCTAGCCATG 122
QY 556 CCCAAGGATGAAGCTGCCACACACTGCTGACTATGTTGCCAAGAGTGGCTTCTTT 615
DB 123 CCCAAGGATGAAGCTGCCACACACTGCTGACTATGTTGCCAAGAGTGGCTTCTTT 182
QY 616 CGGTGTTTCATTGGCTGAATGACCTTTGAAGGGAGGAGACAGTATGTTCAACAGCAAC 675
DB 183 CGGTGTTTCATTGGCTGAATGACCTTTGAAGGGAGGAGACAGTATGTTCAACAGCAAC 242
QY 676 ACTCCACTGAGAACTATAGCAACTGGAATGAGGGGAAACCCAGCGACCCCTATGCTAT 735
DB 243 ACTCCACTGAGAACTATAGCAACTGGAATGAGGGGAAACCCAGCGACCCCTATGCTAT 302
QY 736 GAGGACTGTGTGAGATGCTGAGCTCTGGC 765
DB 303 GAGGACTGTGTGAGATGCTGAGCTCTGGC 332
RESULT 8
CB228545
LOCUS
DEFINITION AGNCOURT 6579990 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5469941
5', mRNA sequence.

```

ACCESSION   BM551435
VERSION     BM551435.1
KEYWORDS    GI:18788488
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1239)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: DCTD/DTF
            CDNA Library Preparation: Rubin Laboratory
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone Distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLOW1975 row: p column: 06
            High quality sequence start: 38
            High quality sequence stop: 301.
            Location/Qualifiers
                1..1239
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:5469941"
                /issue_type="amelanotic melanoma, cell line"
                /lab_host="DH10B (phage-resistant)"
                /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
                EcoRI; CDNA made by oligo-dT priming. Directionally cloned
                into EcoRI/XhoI sites using the following 5' adaptor:
                GGCACGAG(G). Library constructed by Ling Hong in the
                laboratory of Gerald M. Rubin (University of California,
                Berkeley) using LAP-cDNA synthesis kit (Stratagene) and
                Superscript II RT (Life Technologies). Note: this is a
                NIH_MGC Library."

ORIGIN
Query Match      18.4%; Score 153; DB 12; Length 1239;
Best Local Similarity 100.0%; Pred. No. 5.1e-64;
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 GGGCAATATTGCGAAGACTGGGCCCATTTGGGAAGAGGGTGACAAAGGGGAAAAGGTTT 314
Db 137 GGGCAATATTGCGAAGACTGGGCCCATTTGGGAAGAGGGTGACAAAGGGGAAAAGGTTT 196
QY 315 GCTTGGATACCTGGAGAAAAGCAAGCAGGTTACTGTCTGTGATTGTGGAGATACCG 374
Db 197 GCTTGGATACCTGGAGAAAAGCAAGCAGGTTACTGTCTGTGATTGTGGAGATACCG 256
QY 375 GAAATTGTTGGACAACCTGGATATTAGTATTCG 407
Db 257 GAAATTGTTGGACAACCTGGATATTAGTATTCG 289

RESULT 9
R29493
LOCUS       R29493
DEFINITION F1-1006D 22 week old human fetal liver cdna library Homo sapiens
            CDNA clone F1-1006D 5', mRNA sequence.
ACCESSION   R29493
VERSION     R29493.1
KEYWORDS    GI:1511901
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 326)
AUTHORS     Choi,S.S., Yun,J.W., Choi,E.K., Cho,Y.G., Sung,Y.C. and Shin,H.S.

TITLE       Construction of a gene expression profile of a human fetal liver by
            single-pass cDNA sequencing
JOURNAL     Mamm. Genome 6 (9), 653-657 (1995)
MEDLINE     96081342
PUBMED      8535075
COMMENT     Contact: Hee-Sup Shin
            Developmental Genetics
            Pohang Institute of Science & Technology
            San31, Hyodadong Pohang, 790-784 Republic of Korea
            Tel: 562-279-2291
            Fax: 562-279-2199
            Email: shinh@vision.postech.ac.kr
            Seq primer: T3 primer.
            Location/Qualifiers
                1..326
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="F1-1006D"
                /lab_host="X11-blue MRF"
                /clone_lib="22 week old human fetal liver cdna library"
                /note="Vector: pBluescriptII SK(-); Site 1: EcoRI; Site 2:
                XhoI; The cdna library made by oligo-dT primed and
                directionally cloned between 5' Exor I-XhoI3' sites."

ORIGIN
Query Match      17.8%; Score 148; DB 14; Length 326;
Best Local Similarity 100.0%; Pred. No. 1.2e-61;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 569 CTGCCACACACTCATCGCTGACTAGTGTGCCAGAGTGCTCTTTGGGGTTCATTTG 628
Db 1 CTGCCACACACTCATCGCTGACTAGTGTGCCAGAGTGCTCTTTGGGGTTCATTTG 60
QY 629 GCGTGAATGACCTTGAAGAGGGGACAGTACATGTTACACACACACTCCACTGCAGA 688
Db 61 GCGTGAATGACCTTGAAGAGGGGACAGTACATGTTACACACACACTCCACTGCAGA 120
QY 689 ACTATAGCAACTGGAATGAGGGGGAACC 716
Db 121 ACTATAGCAACTGGAATGAGGGGGAACC 148

RESULT 10
LOCUS       CB141360
DEFINITION K-EST0194967 L15CKK1 Homo sapiens cdna clone L15CKK1-30-B10 5',
            mRNA sequence.
ACCESSION   CB141360
VERSION     CB141360.1
KEYWORDS    GI:28116397
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 670)
AUTHORS     Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
            21C Frontier Korean EST Project 2001
            Unpublished (2002)
            Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 30 row: B column: 10
            High quality sequence stop: 670.
            Location/Qualifiers
                1..670
                /organism="Homo sapiens"

TITLE       Construction of a gene expression profile of a human fetal liver by
            single-pass cDNA sequencing
JOURNAL     Mamm. Genome 6 (9), 653-657 (1995)
MEDLINE     96081342
PUBMED      8535075
COMMENT     Contact: Hee-Sup Shin
            Developmental Genetics
            Pohang Institute of Science & Technology
            San31, Hyodadong Pohang, 790-784 Republic of Korea
            Tel: 562-279-2291
            Fax: 562-279-2199
            Email: shinh@vision.postech.ac.kr
            Seq primer: T3 primer.
            Location/Qualifiers
                1..326
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="F1-1006D"
                /lab_host="X11-blue MRF"
                /clone_lib="22 week old human fetal liver cdna library"
                /note="Vector: pBluescriptII SK(-); Site 1: EcoRI; Site 2:
                XhoI; The cdna library made by oligo-dT primed and
                directionally cloned between 5' Exor I-XhoI3' sites."

ORIGIN
Query Match      17.8%; Score 148; DB 14; Length 326;
Best Local Similarity 100.0%; Pred. No. 1.2e-61;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 569 CTGCCACACACTCATCGCTGACTAGTGTGCCAGAGTGCTCTTTGGGGTTCATTTG 628
Db 1 CTGCCACACACTCATCGCTGACTAGTGTGCCAGAGTGCTCTTTGGGGTTCATTTG 60
QY 629 GCGTGAATGACCTTGAAGAGGGGACAGTACATGTTACACACACACTCCACTGCAGA 688
Db 61 GCGTGAATGACCTTGAAGAGGGGACAGTACATGTTACACACACACTCCACTGCAGA 120
QY 689 ACTATAGCAACTGGAATGAGGGGGAACC 716
Db 121 ACTATAGCAACTGGAATGAGGGGGAACC 148

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="L15CKK1-30-B10"
/sex="M"
/cell_line="CK-K1"
/lab_host="Top10P"
/clone_lib="L15CKK1"

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/note="Organ: Liver; Vector: PCNS-D2; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP), and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10P' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

```

ORIGIN
Query Match      17.8%; Score 148; DB 14; Length 670;
Best Local Similarity 99.5%; Pred. No. 1.4e-61;
Matches 198; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 149 GAGATGATGGTGAAGAGAGATCCAGAGAGAGAGAGAGATGGCAAGTGGGACGCA 208
DB 236 GAGATGATGGTGAAGAGAGATCCAGAGAGAGAGAGAGATGGCAAGTGGGACGCA 295
QY 209 TGGGCGGAAAGGATTAAGAGAGAGATCGGTGTATGGGAGATCGGGGCAATATTGGCA 268
DB 296 TGGGCGGAAAGGATTAAGAGAGAGATCGGTGTATGGGAGATCGGGGCAATATTGGCA 355
QY 269 AGACTGGGCGCATTCGGGAGAGAGGTGACAAAGGGGAAAGGTTTGCTTGGGAATACCTG 328
DB 356 AGACTGGGCGCATTCGGGAGAGAGGTGACAAAGGGGAAAGGTTTGCTTGGGAATACCTG 415
QY 329 GAGAAAAAGGCAAGCAGG 347
DB 416 GAGAAAAAGGCAAGCAGG 434

```

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RESULT 11
BX090456
LOCUS
DEFINITION
BX090456 Soares fetal liver spleen INFLS Homo sapiens cDNA clone
IMAGE:998F03662 ; IMAGE:296450, mRNA sequence.
ACCESSION
BX090456
VERSION
BX090456.1 GI:27822119
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 735)
AUTHORS
Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
Radelof,U., Schneider,D. and Korn,B.
Human Unigeneset - RZPD3
Unpublished (2003)
Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD: IMAG998F03662
RZPLIB; I.M.A.G.E. cDNA Clone Collection;
Human Unigeneset - RZPD3 (RZPLIB NO.972)
http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany

```

```

Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTCACAGCAACAGCTATGAC.
Location/Qualifiers
1..735
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAG998F03662 ; IMAGE:296450"
/sex="male"
/dev stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal liver spleen INFLS"
/note="Organ: Liver and Spleen; Vector: p7T3D (Pharmacia)
1st strand cDNA was primed with a Pac I - oligo(dT) primer
[5', AACTGGAAGATTAATAAGATCTTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified p7T3 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."

```

```

FEATURES
source
1..735
Query Match      16.6%; Score 138; DB 13; Length 735;
Best Local Similarity 100.0%; Pred. No. 1.2e-56;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 594 AGCACTGGGATGAGGGGAGCCAGGACCCCTATGTCATGAGGACTGTGTGGAGTG 753
DB 1 AGCACTGGGATGAGGGGAGCCAGGACCCCTATGTCATGAGGACTGTGTGGAGTG 60
QY 754 CTGAGCTCTGCGAGATGGATGACACAGAGTGCATCTTACCATGTACTTTCTGTGTGAG 813
DB 61 CTGAGCTCTGCGAGATGGATGACACAGAGTGCATCTTACCATGTACTTTCTGTGTGAG 120
QY 814 TTCTATCAAGAGAAAAG 831
DB 121 TTCTATCAAGAGAAAAG 138

```

```

RESULT 12
R97480
LOCUS
DEFINITION
R97480 362 bp mRNA linear EST 11-SEP-1995
IMAGE:199539 5' similar to SP:A46466 A46466 MANNOSE-BINDING PROTEIN
A PRECURSOR - ; mRNA sequence.
ACCESSION
R97480
VERSION
R97480.1 GI:983140
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 362)
AUTHORS
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Hollman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaaskis,E., Waterston,R., Williamson,A., Woldmann,P. and
Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
JOURNAL
COMMENT
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1136
High quality sequence stops: 337

```


ORIGIN

Query Match 9.0%; Score 75; DB 10; Length 492;
Best Local Similarity 100.0%; Pred.No.1.3e-25;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 CGTCTACCGCTGAAGTGTGTGCCACACACACAAATTTCCACGAGCCCAAGGAGATGAT 156
|||||
Db 103 CGTCTACCGCTGAAGTGTGTGCCACACACACAAATTTCCACGAGCCCAAGGAGATGAT 162
|||||
QY 157 GGTGAAAAGGAGAT 171
|||||
Db 163 GGTGAAAAGGAGAT 177
|||||

RESULT 15

AV653117 357 bp mRNA linear EST 15-JAN-2002
LOCUS AV653117 GLC Homo sapiens cDNA clone GLCDHE09 3', mRNA sequence.
DEFINITION AV653117
ACCESSION AV653117
VERSION AV653117.1 GI:9874131
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM

REFERENCE
AUTHORS Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 357)

Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
Hu,G., Gu,J., Chen,Z. and Han,Z.
TITLE Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver

Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)

21625106

PUBMED

11752456

COMMENT

Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES

source
1..357
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GLCDHE09"
/tissue_type="corresponding non cancerous liver tissue"
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/lab_host="SOLR"
/clone_lib="GLC"
/note="Vector: pbluescript sk(-); Site 1: EcoRI; Site 2:
XhoI"

ORIGIN

Query Match 8.7%; Score 72; DB 9; Length 357;
Best Local Similarity 100.0%; Pred.No.3.7e-24;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 760 TCTGGCAGATGAATGACACAGAGTGCCATCTTACCATGTACTTGTCTGTGATTCATC 819
|||||
Db 1 TCTGGCAGATGAATGACACAGAGTGCCATCTTACCATGTACTTGTCTGTGATTCATC 60
|||||
QY 820 AAGAAGAAAAG 831
|||||
Db 61 AAGAAGAAAAG 72
|||||

Search completed: March 11, 2004, 19:35:06

Job time : 2537 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model
Run on: March 11, 2004, 16:49:43 ; Search time 3293 seconds
(without alignments)
10937.765 Million cell updates/sec

Title: US-09-600-932-1_COPY_6_836
Perfect score: 831
Sequence: 1 atgaatggcttgcacccctt.....agttcatcaagaagaaaag 831

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:
1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*
15: em.ba.*
16: em.fun.*
17: em.hum.*
18: em.in.*
19: em.mu.*
20: em.om.*
21: em.or.*
22: em.ov.*
23: em.pat.*
24: em.ph.*
25: em.pl.*
26: em.ro.*
27: em.sts.*
28: em.un.*
29: em.vi.*
30: em.hg.hum.*
31: em.hg.inv.*
32: em.hg.other.*
33: em.hg.mus.*
34: em.hg.pln.*
35: em.hg.rod.*
36: em.hg.nam.*
37: em.hg.vrt.*
38: em.sy.*
39: em.hgo.hum.*
40: em.hgo.mus.*
41: em.hgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	831	100.0	1594	9	AB002631 Homo sapi
2	831	100.0	1595	6	E29008 Novel colle
3	826.2	99.4	1016	6	AX376032 Sequence
4	826.2	99.4	1016	9	AY359038 Homo sapi
5	642.8	77.4	867	10	AB016429 Mus muscu
6	390	46.9	141262	9	AC080033 Homo sapi
7	390	46.9	182475	2	AC023487 Homo sapi
8	321.8	38.7	234922	2	AC097055 Rattus no
9	313.8	37.8	168900	2	AC115924 Mus muscu
10	313.8	37.8	22510	2	AC123656 Mus muscu
11	313.8	37.8	345420	2	AC131337 Mus muscu
12	265.4	31.9	1272	5	BC056052 Xenopus l
13	244.6	29.4	813	6	BD103332 Novel col
14	244.6	29.4	1238	6	AR252616 Sequence
15	244.6	29.4	1238	6	AX403469 Sequence
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17	244.6	29.4	1238	6	AX491060 Sequence
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19	244.6	29.4	1248	9	BC000078 Homo sapi
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21	239	28.8	813	6	BD103338 Novel col
22	239	28.8	1522	6	BD103307 Novel col
23	233.8	28.1	735	6	BD103333 Novel col
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32	202	24.3	663	6	BD103337 Novel col
33	202	24.3	1067	6	BD103306 Novel col
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35	180	22.9	1197	6	BD103329 Novel col
36	188	22.6	591	6	BD103335 Novel col
37	188	22.6	995	6	BD103304 Novel col
38	171.4	20.6	477	6	BD103334 Novel col
39	155.6	18.7	139357	9	AC010907 Homo sapi
40	154.8	18.6	246539	2	AC125638 Rattus no
41	153.6	18.5	147414	9	AC107953 Homo sapi
42	153.6	18.5	182475	2	AC023487 Homo sapi
43	151.6	18.2	175475	2	AC123631 Mus muscu
44	147.4	17.7	212049	5	EX005484 Zebrafish
45	111.6	13.4	151321	2	AC136264 Rattus no

ALIGNMENTS

RESULT 1
LOCUS AB002631 1594 bp mRNA linear PRI 24-JUN-1999
DEFINITION Homo sapiens mRNA for collectin 34, complete cds.
ACCESSION AB002631
VERSION AB002631.1 GI:5162874
KEYWORDS collectin 34.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (sites)
Ohtani,K., Suzuki,Y., Eda,S., Kawai,T., Kase,T., Yamazaki,H.,
Keshi,H., Sakai,Y., Fukuh,A., Sakamoto,T. and Wakamiya,N.
AUTHORS
TITLE Molecular cloning of a novel human collectin from liver (CL-L1)

J. Biol. Chem. 274 (19), 13681-13689 (1999)
 99240768
 MEDLINE
 PUBMED
 REFERENCE 2 (bases 1 to 1594)
 AUTHORS Ohtani, K.
 TITLE Direct Submission
 JOURNAL Submitted (04-APR-1997) Katsuki Ohtani, Osaka Prefectural Institute of Public Health, Department of Pathology; 3-69, Nakamichi 1-chome Higashinari-ku, Osaka, Osaka 537, Japan
 (E-mail: suzuki@iph.pref.osaka.jp, Tel: +81-6-972-1321, Fax: +81-6-972-0772)
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 Best Local Similarity 100.0%; Pred. No. 2.9e-198;
 Matches 831; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATCAATGGCTTTGCACTCTTCTGCTGCAAGAACCAATTTATCTCTCGGACTATTTCTT 60
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 QY 661 ATGTTTCACAGACAACTCCACTGCAGACTATAGCAACTTGGAAATGAGGGGAAACCCAGC 720
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 QY 781 GAGTGGCATCTTACCATGTACTTTGTCTGTGAGTTTCATCAAGAGAGAAAAG 831
 DB 786 GAGTGGCATCTTACCATGTACTTTGTCTGTGAGTTTCATCAAGAGAGAAAAG 836
 RESULT 2
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 LOCUS E29008 1595 bp DNA linear PAT 18-JUN-2001
 DEFINITION Novel collectin.
 ACCESSION E29008
 VERSION E29008.1 GI:113018416
 KEYWORDS JP 1999206377-A/1.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1595)
 AUTHORS Nobutaka, W.
 TITLE Novel collectin
 JOURNAL Patent: JP 1999206377-A 1 03-AUG-1999;
 FUSO YAKUHIN KOGYO KK
 COMMENT OS Homo sapiens (human)
 PN JP 1999206377-A/1
 PD 03-AUG-1999
 PF 23-JAN-1998 JP 1998011281
 PR NOBUTAKA WAKAMIYA
 PI C12N15/09, C07K14/47, C07K14/78, C12P21/00, C12N15/00 CC
 PC Strandedness: Double;
 CC Topology: Linear;
 FH Key Location/Qualifiers
 FT CDS 6..836.
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 Best Local Similarity 100.0%; Pred. No. 2.9e-198;
 Matches 831; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGATGGCTTTGCACTCTTCTGCTGCAAGAACCAATTTATCTCTCGGACTATTTCTT 60
 DB 6 ATGATGGCTTTGCACTCTTCTGCTGCAAGAACCAATTTATCTCTCGGACTATTTCTT 65
 QY 61 TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCGCTCTACCGCTGAAGTCTGTGCC 120
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 DB 126 ACACACACAAATTCACAGACGCCAAGAGAGATGATGTTGAAAAGAGATCCAGAGGAA 185
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RESULT 3
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 LOCUS AX376032 1016 bp DNA linear PAT 01-MAR-2002
 DEFINITION Sequence 99 from Patent WO0168848.
 ACCESSION AX376032
 VERSION AX376032.1 GI:19170408
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 Baker, K.P., Chen, J., Desnoyers, L., Goddard, A., Godowski, P.J.,
 Gurney, A.L., Pan, J., Smith, V., Watanabe, C.K., Wood, W.I. and
 Zhang, Z.
 Secreted and transmembrane polypeptides and nucleic acids encoding
 the same
 Patent: WO 0168848-A 99 20-SEP-2001;
 Genentech, Inc. (US)
 Location/Qualifiers
 1..1016
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ORIGIN
 Query Match 99.4%; Score 826.2; DB 6; Length 1016;
 Best Local Similarity 99.6%; Pred. No. 4.7e-197;
 Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 ATGATGCTTGTGATCCTTCTGAGAGAACCAATTTATCTCTCTGGTACTATTCTT 60
 Db 22 ATGATGCTTGTGATCCTTCTGAGAGAACCAATTTATCTCTCTGGTACTATTCTT 81

Qy 61 TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCGCTCTTACCGCTGAAGTCTTGCC 120
 Db 82 TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCGCTCTTACCGCTGAAGTCTTGCC 141
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 Db 142 ACACACAAATTTCCACGAGCCCAAGGAGATGATGTTGMAAAGGAGATCCAGAGAA 201
 Qy 181 GAGGAAAGCATGCAAAAGTGGGACGATGGGCGGAAAGGAATTTAAAGGAGAACTGGGT 240
 Db 202 GAGGAAAGCATGCAAAAGTGGGACGATGGGCGGAAAGGAATTTAAAGGAGAACTGGGT 261
 Qy 241 GATATGGAGATCGGGCAATATTGGCAAGACTGGGCCCATTTGGGAGAGGGGTGACAA 300
 Db 262 GATATGGAGATCGGGCAATATTGGCAAGACTGGGCCCATTTGGGAGAGGGGTGACAA 321
 Qy 301 GGGGAAAAGGTTTGTCTTGAATACCTTGGAGAAAAGGCAAGCAGGTACTGTCTGTGAT 360
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 Qy 361 TGTGGAAGATACCGGAAATTTGTTGGCACTGCGATATTAGTATTTCCCGGCTCAAGACA 420
 Db 382 TGTGGAAGATACCGGAAATTTGTTGGCACTGCGATATTAGTATTTCCCGGCTCAAGACA 441
 Qy 421 TCTATGAAGTTTGTCAAGATGTGATAGCAGGATTTAGGAAAACCTGAAGAGAAATTTCTAC 480
 Db 442 TCTATGAAGTTTGTCAAGATGTGATAGCAGGATTTAGGAAAACCTGAAGAGAAATTTCTAC 501
 Qy 481 TACATCTGTCAGGAGAGAACTACAGGAAATCCCTAACCCACTGCAGGATTCGGGGT 540
 Db 502 TACATCTGTCAGGAGAGAACTACAGGAAATCCCTAACCCACTGCAGGATTCGGGGT 561
 Qy 541 GGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACACACTCATCGCTACTATGTTGCC 600
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RESULT 4
 AX359038
 LOCUS AX359038 1016 bp mRNA linear PRI 03-OCT-2003
 DEFINITION Homo sapiens clone DNA50980 COLEC10 (UNQ366) mRNA, complete cds.
 ACCESSION AX359038
 VERSION AX359038.1 GI:37183193
 KEYWORDS FLI CDNA.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 1016)
 Clark, H.F., Gurney, A.D., Abaya, E., Baker, K., Baldwin, D., Brush, J.,
 Chen, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B.,
 Dowd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, Q., Hase, P.E.,
 Heldens, S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S.,
 Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C.,
 Schoenfeld, J., Seshagiri, S., Simmons, L., Singh, J., Smith, V.,
 Stinson, J., Vagts, A., Vandlen, R., Watanabe, C., Wiand, D., Woods, K.,

Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
Goddard,A., Wood,W.I. and Godowski,P.
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins:
A Bioinformatics Assessment
Genome Res. 13 (10), 2265-2270 (2003)
12975309
2 (bases 1 to 1016)
Clark,H.F.
Direct Submission
Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA
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Best Local Similarity 99.6%; Pred No. 4.7e-197;
Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ATGAATGGCTTTGGCATCTTCTGCTCGAAGAACCAATTTATCTCTCGTACTATTCTT 60
DB 22 ATGAATGGCTTTGGCATCTTCTGCTCGAAGAACCAATTTATCTCTCGTACTATTCTT 81
QY 61 TTGCAAAATTCAGAGCTGGCTGTGATATTCATAGCCGCTACCGCTGAAGTCTGTGCC 120
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Db 502 TACATCGTCAGGAGAGAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGGGGT 561
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DB 562 GGAATGCTAGCAATGCCCAAGGATGAAGCTGCCACACACTCATCGCTGACTATTTGCC 621
QY 601 AAGAGTGGCTTTCTTTTCGGGTGTTTCATTGTCGCTGAATGACCTTGAAGGGAGGACAGTAC 660
DB 622 AAGAGTGGCTTTCTTTTCGGGTGTTTCATTGTCGCTGAATGACCTTGAAGGGAGGACAGTAC 681
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QY 781 GAGTGCCATCTTACCATGTACTTTGCTGTGAGTTTCATCAAGAAGAAAAG 831
DB 802 GAGTGCCATCTTACCATGTACTTTGCTGTGAGTTTCATCAAGAAGAAAAG 852
RESULT 5
AB016429 867 bp mRNA linear ROD 07-JAN-2003
LOCUS Mus musculus mRNA for collectin-L1, complete cds.
DEFINITION
AB016429
ACCESSION
AB016429.1 GI:27530340
VERSION
collectin-L1.
KEYWORDS
Mus musculus (house mouse)
SOURCE
Mus musculus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
Kawai,T., Suzuki,Y., Eda,S., Kase,T., Ohtani,K., Sakai,Y.,
Keshi,H., Fukuoh,A., Sakamoto,T., Nozaki,M., Copeland,N.G.,
Jenkins,N.A. and Wakamiya,N.
Molecular cloning of mouse collectin liver 1
Biosci. Biotechnol. Biochem. 66 (10), 2134-2145 (2002)
2333927
MEDLINE
12450124
REFERENCE
2 (bases 1 to 867)
Kawai,T. and Suzuki,Y.
Direct Submission
Submitted (21-JUL-1998) Takao Kawai, Osaka Prefectural Institute of
Public Health, Laboratory of Food Microbiology, 3-69 Nakamichi
1-chome, Higashinari-ku, Osaka 537-0025, Japan
(E-mail:kawai@ph.pref.osaka.jp, Tel:81-6-972-1321,
Fax:81-6-972-2393)
Location/Qualifiers
1. 867
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Query Match 77.4%; Score 642.8; DB 10; Length 867;
Best Local Similarity 85.9%; Pred. No. 6.8e-151;

Matches	713;	Conservative	0;	Mismatches	117;	Indels	0;	Gaps	0;
QY	1	ATGAATGGCTTTGGCATCTCTGCTTCCGAGAAACCAATTAATTCCTCCTGCTGACTATTTCTT	60						
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QY	181	GAGGGAAGCATGGCAAGTGGAGCGCATGCGGCGGCGAAGAAATTAAGAGACTGGGT	240						
Db	189	GAGGCAAGATGGCAAGTGGAGCGCCAGGAGCAAAAGAGGTGAAAGAGAGCTGGT	248						
QY	241	GATATGGGAGATCGGGGCAATATTTGGCAAGACTGGGCCCATTTGGGAAGAGGTGACAAA	300						
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QY	361	TGTGGAAGATACCGGAATTTGTTGGCAACTGGATATTAGTATTTGCCCGCTCAAGACA	420						
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QY	421	TCTATGAAGTTTGTCAAGATGTGATAGCAGGGATTAGGAAAATGGAAGAGAAATTTCTAC	480						
Db	429	TCAATGAATTCATCAAGATGTTATAGCAGGGATCCGGGAAATGGAAGAGAAATTTCTAC	488						
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LOCUS	AC080033								
DEFINITION	Homo sapiens chromosome 8, clone RP11-895J16, complete sequence.								
ACCESSION	AC080033								
VERSION	AC080033.10								
KEYWORDS	HTG.								
SOURCE	Homo sapiens (human)								
ORGANISM	Homo sapiens								
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.								
TITLE	1 (bases 1 to 141262)								

JOURNAL
REFERENCE
AUTHORS

Unpublished
2 (bases 1 to 141262)

Biren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Beda, F., Boguslavskiy, L.,
Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A.,
Chepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
Dearlano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferreira, P.,
Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M.,
Graham, L., Grand-Pierre, N., Hagos, B., Hearford, A., Horton, L.,
Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., LaRocque, K.,
Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lieff, C., Liu, G.,
Macdonald, P., Marquis, N., McCarty, M., McEwan, P., McKernan, K.,
McPheters, R., Meldrum, J., Meneus, L., Mihova, T., Mlenga, V.,
Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T.,
O'Donnell, P., O'Neill, D., Oliver, T.M., Oliver, J., Peterson, K.,
Pierre, N., Pisani, C., Pollara, V., Raymond, C., Rieback, M., Riley, R.,
Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P.,
Sougnuez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J.,
Tirell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A.,
Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J.,
Zimmer, A. and Zody, M.

TITLE
JOURNAL
REFERENCE
AUTHORS

Direct Submission
Submitted (23-SEP-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 141262)

Biren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Boguslavskiy, L., Boukhgalter, B.,
Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,
Chepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, A.,
Cooke, P., Dearlano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S.,
Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S.,
Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N.,
Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kanat, A., Karatas, A., Kella, C., LaRocque, K., Lamazares, R.,
Landers, T., Lehoczy, J., Levine, R., Liu, G., MacLean, C.,
Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M.,
McEwan, P., McKernan, K., Meldrum, J., Meneus, L., Mihova, T.,
Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.,
Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J.,
Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C.,
Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J.,
Rosetti, M., Roy, A., Santos, R., Schauer, S., Schuback, R., Seaman, S.,
Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE
JOURNAL
REFERENCE
AUTHORS

Direct Submission
Submitted (15-FEB-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
4 (bases 1 to 141262)

Biren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Boguslavskiy, L., Boukhgalter, B.,
Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,
Chepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, A.,
Cooke, P., Dearlano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S.,
Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S.,
Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N.,
Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kanat, A., Karatas, A., Kella, C., LaRocque, K., Lamazares, R.,
Landers, T., Lehoczy, J., Levine, R., Liu, G., MacLean, C.,
Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M.,
McEwan, P., McKernan, K., Meldrum, J., Meneus, L., Mihova, T.,
Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.,
Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J.,
Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C.,
Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J.,
Rosetti, M., Roy, A., Santos, R., Schauer, S., Schuback, R., Seaman, S.,
Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Topham, K., Travers, M., Travis, N., Trigilio, J., Testaye, S., Theodore, J.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
 Direct Submission
 Submitted (20-FEB-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Feb 20, 2002 this sequence version replaced gi:18653568.
 All repeats were identified using RepeatMasker:
 Smit, A.P.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html
 ----- Genome Center -----
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information -----
 Center project name: L10939
 Center clone name: 885_J16

FEATURES

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Matches 390;	Conservative	0;	Mismatches 0;	Indels 0;
Gaps	0;			

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RESULT 7
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LOCUS Homo sapiens chromosome 8 clone RP11-164H21, WORKING DRAFT
DEFINITION SEQUENCE, 3 unordered pieces.
AC023487
AC023487 GI:13357236
HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP; HTGS_ACTIVEFIN.
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 182475)
Abola, A.P., Bruno, D., Conn, L., Della Rosa, M., Faulkner, D.,
Fedorov, S., Hansen, N., Hyman, R., Mao, J., Marathe, R.,
Mao, J., Kemp, C., Kortler, S., Lam, B., Marathe, R., Miranda, M.,
Morsehouse, A.J., Nguyen, M., Oefner, P., Palm, C.J., Ramirez, D.,
Southwick, A.M., Webb, C., Wilhelm, J., Yu, S., and Davis, R.W.
Unpublished
2 (bases 1 to 182475)
Bruno, D., Conn, L., Della Rosa, M., Faulkner, D., Federspiel, N.,
Glukhov, S., Hansen, N., Hyman, R., Mao, J., Marathe, R.,
Morsehouse, A.J., Oefner, P., Palm, C.J., Ramirez, D.,
Yu, S., and Davis, R.W.
Direct Submission
Submitted (14-FEB-2000) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
USA
On Mar 16, 2001 this sequence version replaced gi:13324778.
----- Genome Center
Center: Stanford DNA Sequencing and Technology Development
Center
Center code: SOSTDC
Web site: http://sequence-www.stanford.edu/group/human/
Contact: hum-info@sequence.stanford.edu
----- Project Information
Center project name: 844
Center clone name: RP11-164H21
----- Summary Statistics
Sequencing Vector: M13mp18; X0513; 98% of reads
Sequencing Method: plasmid; plasmid accession; 2% of reads
Chemistry: Dye-terminator Big Dye; 99% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 180260 bases at least Q40
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Consensus quality: 180507 bases at least Q20
Insert size: 178614; agarose-fp
Insert size: 182275; sum-of-contigs
Quality coverage: 8.1x in Q20 bases; agarose-fp
Quality coverage: 7.9x in Q20 bases; sum-of-contigs.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 42072: contig of 42072 bp in length
* 42073 42172: gap of unknown length
* 42173 109254: contig of 67082 bp in length
* 109255 109354: gap of unknown length
* 109355 182475: contig of 73121 bp in length.
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/chromosomes="8"

FEATURES
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LOCUS Rattus norvegicus clone CH230-2P22, WORKING DRAFT SEQUENCE, 3
DEFINITION Rattus norvegicus (Norway rat)
ACCESSION AC097055
VERSION AC097055.5 GI:25007102
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 234922)
Munzy, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C.,
Albrooks, S.L., Amaratunga, H.C., Aze, J.R., Ayele, M., Banks, T.,
Barbacia, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D.,
Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P.,
Buhay, C., Burck, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
Carroll, T.P., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,
Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,
Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
Gabisli, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
```

Correll, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hughes, M., Holloway, C., Hollins, B., Homs, F., Howard, S., Huber, J., Huly, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louleseg, H., Lorado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maneshwar, M., Mapus, P., Martin, R., Martindale, A., Martinez, B., Massey, E., Mawhrey, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, S., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savary, G., Scherer, S., Scott, G., Shen, H., Shoostari, N., Sisson, I., Sodergren, S., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstein, G., and Gibbs, R.

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: TUIS
Center clone name: CH230-2F22
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 231210 bases at least Q40
Consensus quality: 232236 bases at least Q30
Consensus quality: 233086 bases at least Q20
Estimated insert size: 241867; sum-of-contigs estimation
Quality coverage: 11x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces

* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 188689: contig of 188689 bp in length
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* /mol_type="genomic DNA"
* /db_xref="taxon:10116"
* /clone="CH230-2F22"

FEATURES

source

ORIGIN

Query Match 38.7%; Score 321.8; DB 2; Length 234922;
Best Local Similarity 89.2%; Pred. No. 3.2e-70;
Matches 347; Conservative 0; Mismatches 42; Indels 0; Gaps 0;
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DB 14603 TGTGTGAGATGCTGAGCTCTGGCAGATGGAATGACACAGAGTGGCCATCTTACCATGTAT 14662
QY 802 TTTGCTGTGAGTTTCATCAAG 830
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RESULT 9

AC115924

LOCUS

DEFINITION

AC115924

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
 Fato, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S.,
 Glade, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
 Hagos, B., Horton, L., Kellis, M., Iliev, I., Johnson, R., Jones, C.,
 Kanat, A., Karatas, A., Kelle, C., Lacroque, K., Lamazares, R.,
 Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K., Liu, G.,
 Maclean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C.,
 McCarthy, M., McSwan, P., McKernan, K., Meldrum, J., Menes, L.,
 Mihova, T., Mienna, V., Murphy, J., Naylor, J., Nguyen, C., Nicol, R.,
 Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D.,
 Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
 Raymond, C., Rettig, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
 Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R.,
 Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
 Straus, K., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
 Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
 Viel, R., Vo, R., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
 Zainoun, J., Zemdek, L., Zimmer, A. and Zody, M.

Direct Submission
 Submitted (22-MAR-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 166900)

Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T.,
 Boguslavsky, L., Boukhgelter, B., Camarata, J., Chang, J., Choepel, Y.,
 Collymore, A., Cook, A., Cooke, P., Corum, B., Dearellano, K.,
 Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Fato, S.,
 Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S.,
 Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B.,
 Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
 Kanat, A., Karatas, A., Kellis, C., Landers, T., Levine, R.,
 Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., Maclean, C.,
 Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M.,
 Meldrum, J., Menes, L., Mihova, T., Mienna, V., Murphy, T., Naylor, J.,
 Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P.,
 O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
 Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P.,
 Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C.,
 Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,
 Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M.,
 Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, R., Wilson, B., Wu, X.,
 Wyman, D., Young, G., Zainoun, J., Zemdek, L., Zimmer, A. and Zody, M.

Direct Submission
 Submitted (18-JUN-2003) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Jun 18, 2003 this sequence version replaced gi:21490462.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIER
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L24895
 Center clone name: 511_0_11
 ----- Summary Statistics
 Sequencing vector: plasmid; n/a; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 165673 bases at least Q40
 Consensus quality: 166156 bases at least Q30
 Consensus quality: 166365 bases at least Q20
 Insert size: 157000; agarose-fp
 Insert size: 166600; sum-of-contigs
 Quality coverage: 13.2 in Q20 bases; agarose-fp
 Quality coverage: 12.4 in Q20 bases; sum-of-contigs

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 4 contigs. Gaps between the contigs
 * are represented as runs of N. The order of the pieces
 * is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have
 * provided by the submitter.
 * This sequence will be replaced.
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.

1 48320: contig of 48320 bp in length
 * 48321 48420: gap of 100 bp
 * 48421 59799: contig of 11379 bp in length
 * 59800 59899: gap of 100 bp
 * 59900 135830: contig of 75931 bp in length
 * 135831 135930: gap of 100 bp
 * 135931 166900: contig of 30970 bp in length.

FEATURES
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 /clone_lib="RP24-S11011"
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 /notes="assembly_fragment
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 vector_side:left"
 misc_feature
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 /note="assembly_fragment"
 misc_feature
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 135931..166900
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 clone_end:T7
 vector_side:right"

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 Best Local Similarity 87.9%; Pred. No. 3.4e-68;
 Matches 342; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 442 GTGATGACAGGGATTAGGAACTGGAAGAGAAATTTACTACTACATCGTCGAGGAGAGAGAG 501
 Db 15148 GTTATAGCAGGATCCGGAACTGAAGAGAAATTTACTACTATTTGTGCGAGGAGAGAG 15207

QY 502 AACTACAGGGAATCCCTAACCCACTCCAGATTCGGGGTGGGAATCGTACCCATGCCCAAG 561
 Db 15208 AACTACAGGGAATCTCTGACCCACTCCAGATTCGGAGGAGGATGCTAGCCATGCCCAAG 15267

QY 562 GATGAGCTCCCAACACATCATCTGCTGACTATGTTGCCAAGAGTGGCTTCTTTTCGGGTG 621
 Db 15268 GATGAGTCTGTTAACACCCCTTATGCTGACTATGTCGCAAGAGTGGTTTCTTCAGAGTG 15327

QY 622 TTCAATTCGCTGATGATGACCTTGAAAGGGAGGAGGACAGTACATGTTTACAGACACACTCCA 681
 Db 15328 TTCAATTCGCTGATGATGACCTTGAGAGGGAGGAGGCAATATGTTTACAGATTAACACTCCA 15387

QY 682 CTGACAGAACTATAGCACTGGAAATGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 741
 Db 15388 TTGACAGAACTATAGCACTGGAAATGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 15447

QY 742 TGTGTGAGATGCTGAGCTCTGGCAGATGGAATGACACAGAGTGGCATCTTACCATGTAC 801
 Db 15448 TGTGTGAGATGCTGAGCTCTGGCAGATGGAATGACACAGAGTGGCATCTTACCATGTAT 15507

QY 802 TTTGTTCTGTGAGTTTCATCAAG 830
 Db 15508 TTTGTTCTGTGAGTTTGTCAAG 15536

RESULT 10
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 LOCUS AC123656 Mus musculus clone RP23-188M21, WORKING DRAFT SEQUENCE, 6 unordered
 DEFINITION pieces.
 ACCESSION AC123656
 VERSION AC123656.6 GI:29294284

HTG; HTGS PHASE1; HTGS_DRAFT.
Mus musculus (house mouse)
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 222510)
Biren, B., Nusbaum, C. and Lander, E.
Mus musculus, clone RP23-188M21
Unpublished
2 (bases 1 to 222510)
Biren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Bouckgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J. S., Dodge, S., Fero, S., Ferreira, P., Fitzgerald, M., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRoque, K., Lanazares, R., Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Menues, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupack, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, J., Strauss, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (01-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 222510)
Biren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, S., Arachchi, H. M., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Bouckgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., Dearellano, K., Diaz, J. S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Fero, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Menues, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupack, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V. S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (27-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 27, 2003 this sequence version replaced gi:28626869.
All repeats were identified using RepeatMasker:
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIER
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L26354
Center clone name: 188 M21
----- Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 221635 bases at least Q40
Consensus quality: 221908 bases at least Q30
Consensus quality: 221986 bases at least Q20
Insert size: 20000; agarose-fp
Insert size: 222010; sum-of-contigs
Quality coverage: 10.7 in Q20 bases; agarose-fp
Quality coverage: 9.6 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
* 1 2031: contig of 2031 bp in length
* 2032 2131: gap of 100 bp
* 2132 15244: contig of 13113 bp in length
* 15245 15344: gap of 100 bp
* 15345 37649: contig of 22305 bp in length
* 37650 37749: gap of 100 bp
* 37750 148102: contig of 110353 bp in length
* 148103 148202: gap of 100 bp
* 148203 190361: contig of 42159 bp in length
* 190362 190461: gap of 100 bp
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ORIGIN
Query Match 37.8%; Score 313.8; DB 2; Length 222510;
Best Local Similarity 87.9%; Pred. No. 3.3e-68;
Matches 342; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
QY 442 GTGATACAGGAGTATAGGAACTGAGAGAAATCTACTACTCTCAGAGAGAGAG 501
Db 157200 GTTATAGCAGGATCCGGGAACTGAGAGAAATCTACTACTCTCAGAGAGAGAG 157259
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Db 157260 AACTACAGGAAATCTCTGACCCACTGCAGATTCGGGGTGGAAATCTAGCCATGCCCAAG 157319
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Db 157320 GATGAGCTGTTAAACCCCTTATGCTGACTATGCGCGAGAGTGGTTCCTCAGAGTG 157379
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QY 682 CTGCAGACTATAGCACTGGATGAGGGGGGAGCCAGGACCCCTATGCTCATGAGGAC 741

TITLE
JOURNAL
REFERENCE
AUTHORS

```

Db 157440 TTGCAGAACTACAGCAACTGGAGGAGGAGGAACTAGTACCCTCGGGCCATGAGGAC 157499
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Db 157500 TGTGTGGATGTTGAGCTCTGGAGGTTGGAATGACACAGAGTGTCACCTTACCATGTAT 157559
QY 802 TTGTGCTGTGAGTTTCATCAAGAAGAAAA 830
Db 157560 TTGTGCTGTGAGTTTGTCAAGAAGAAAA 157588

RESULT 11
AC131337
LOCUS
DEFINITION
AC131337 345420 bp DNA linear HTG 23-APR-2003
MUS musculus clone RP23-480E1, WORKING DRAFT SEQUENCE, 17 unordered
pieces.
ACCESSION
AC131337 4 GI:30017797
VERSION
HTG; HTGS PHASE1; HTGS_DRAFT.
KEYWORDS
MUS musculus (house mouse)
SOURCE
MUS musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 345420)
Birken.B., Nusbaum.C. and Lander.E.
MUS musculus, clone RP23-480E1
Unpublished
2 (bases 1 to 345420)
Birken.B., Nusbaum.C., Lander.E., Ali.A., Allen.N., Anderson.S.,
Barna.N., Bastien.V., Bloom.T., Boguslavskiy.L., Boukhgalter.B.,
Camara.J., Chang.J., Chazaro.B., Choepel.Y., Collymore.A.,
Cook.A., Cooke.P., DeArelano.K., Dewar.K., Diaz.J.S., Dodge.S.,
Faro.S., Ferreira.P., Fitzgerald.M., Gage.D., Galagan.J.,
Gardyna.S., Gord.S., Graham.L., Grand-Pierre.N., Hagos.B.,
Horton.L., Hulme.W., Iliev.I., Johnson.R., Jones.C., Kamat.A.,
Karatas.A., Kells.C., Landers.T., Levine.R., Lindblad-Toh.K.,
Liu.G., MacLean.C., Macdonald.P., Major.J., Matthews.C.,
McCarthy.M., Meldrum.J., Meneus.L., Mihova.T., Mienga.V.,
Murphy.T., Naylor.J., Nguyen.C., Nicol.R., Norbu.C., Norman.C.H.,
O'Connor.T., O'Donnell.P., O'Neil.D., Oliver.J., Peterson.K.,
Phunkhang.P., Pierre.N., Raymond.C., Retta.R., Rise.C., Rogov.P.,
Roman.J., Roy.A., Schauer.S., Schuback.R., Seaman.S., Severy.P.,
Smith.C., Spencer.B., Stange-Thomann.N., Stojanovic.N., Talamas.J.,
Testaye.S., Theodore.J., Topham.K., Travers.M., Vassiliev.H.,
Viel.R., Vo.A., Wilson.B., Wu.X., Wyman.D., Young.G., Zainoun.J.,
Zembek.L., Zimmer.A. and Zody.M.
Direct Submission
Submitted (20-AUG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 345420)
Birken.B., Nusbaum.C., Lander.E., Abouelleil.A., Allen.N.,
Anderson.S., Arachchi.H.M., Barna.N., Bastien.V., Bloom.T.,
Boguslavskiy.L., Boukhgalter.B., Camara.J., Chang.J., Choepel.Y.,
Collymore.A., Cook.A., Cooke.P., Corum.B., DeArelano.K.,
Diaz.J.S., Dodge.S., Dooley.K., Dorris.L., Erickson.J., Faro.S.,
Ferreira.P., Fitzgerald.M., Gage.D., Galagan.J., Gardyna.S.,
Graham.L., Grand-Pierre.N., Hagos.B., Hagopian.D., Hagos.B.,
Hall.J., Horton.L., Hulme.W., Iliev.I., Johnson.R., Jones.C.,
Kamat.A., Karatas.A., Kells.C., Landers.T., Levine.R.,
Lindblad-Toh.K., Liu.G., Lui.A., Mabbitt.R., MacLean.C.,
Macdonald.P., Major.J., Manning.J., Matthews.C., McCarthy.M.,
Meldrum.J., Meneus.L., Mihova.T., Mienga.V., Murphy.T., Naylor.J.,
Nguyen.C., Nicol.R., Norbu.C., O'Connor.T., O'Donnell.P.,
O'Neil.D., Oliver.J., Peterson.K., Phunkhang.P., Pierre.N.,
Rachupka.A., Ramasamy.U., Raymond.C., Retta.R., Rise.C., Rogov.P.,
Roman.J., Schauer.S., Schuback.R., Seaman.S., Severy.P., Smith.C.,
Spencer.B., Stange-Thomann.N., Stojanovic.N., Stubbs.M.,
Talamas.J., Testaye.S., Theodore.J., Topham.K., Travers.M.,
Vassiliev.H., Venkataraman.V.S., Viel.R., Vo.A., Wilson.B., Wu.X.,
Wyman.D., Young.G., Zainoun.J., Zembek.L., Zimmer.A. and Zody.M.
Direct Submission
Submitted (23-APR-2003) Whitehead Institute/MIT Center for Genome

```

COMMENT

Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Apr 17, 2003 this sequence version replaced gi:28626850.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L26504
 Center clone name: 480_E_1

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 17 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1 1221: contig of 1221 bp in length
 * 1222: gap of 100 bp
 * 1322 2740: contig of 1419 bp in length
 * 2741 2840: gap of 100 bp
 * 2841 4351: contig of 1511 bp in length
 * 4352 4451: gap of 100 bp
 * 4452 7231: contig of 2780 bp in length
 * 7232 7331: gap of 100 bp
 * 7332 13580: contig of 6249 bp in length
 * 13581 13680: gap of 100 bp
 * 13681 13224: contig of 5544 bp in length
 * 13225 13324: gap of 100 bp
 * 13325 24245: contig of 4921 bp in length
 * 24246 24345: gap of 100 bp
 * 24346 33304: contig of 8959 bp in length
 * 33305 33404: gap of 100 bp
 * 33405 43959: contig of 10555 bp in length
 * 43960 44059: gap of 100 bp
 * 44060 64192: contig of 20133 bp in length
 * 64193 64292: gap of 100 bp
 * 64293 140233: contig of 75941 bp in length
 * 140234 140333: gap of 100 bp
 * 140334 166937: contig of 26604 bp in length
 * 166938 167037: gap of 100 bp
 * 167038 202564: contig of 35527 bp in length
 * 202565 202664: gap of 100 bp
 * 202665 235865: contig of 33201 bp in length
 * 235866 282239: contig of 46274 bp in length
 * 282240 282339: gap of 100 bp
 * 282340 325240: contig of 42901 bp in length
 * 325241 345240: gap of 100 bp
 * 345241 345420: contig of 20080 bp in length.

FEATURES

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misc_feature

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misc_feature

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misc_feature

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 /note="assembly_fragment"
 282340..325240
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 325341..345420
 /note="assembly_fragment
 clone_end:17
 vector_side:right"

ORIGIN

Query Match 37.8%; Score 313.8; DB 2; Length 345420;
 Best Local Similarity 87.9%; Pred. No. 3.3e-68;
 Matches 342; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
 QY 442 GTGATAGCAGGGATTAGGAAACTGAGAGAAATTTACTACATCGTCGAGAGAGAG 501
 Db 176225 GTTATAGCAGGGATCGGGAAACTGAGAGAAATTTACTACATCGTCGAGAGAGAG 176284
 QY 502 AACTAGAGGAATCCTTACCCACTCGAGATCGGGTGGGATCTAGCCATGCCCAAG 561
 Db 176285 AACTAGAGGAATCCTTACCCACTCGAGATCGGGTGGGATCTAGCCATGCCCAAG 176344
 QY 562 GATGAAGCTGCCAACACACTCATCGTCTACTATGTTGCCAAGAGTGGTCTTTTGGGGT 621
 Db 176345 GATGAAGCTGTTAACACCTTATGTTGCTACTATGTTGCCAAGAGTGGTCTTTTGGGGT 176404
 QY 622 TTGATGGCTGATGATGACCTTGAAGGGAGGACAGTACATGTTTACAGACACACTTCCA 681
 Db 176405 TTGATGGCTGATGATGACCTTGAAGGGAGGACAGTACATGTTTACAGACACACTTCCA 176464
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 QY 742 TGTGTGAGATGCTGAGCTCTGCGAGATGAGATGACACAGATGCGATTTACCATGTAC 801
 Db 176525 TGTGTGAGATGCTGAGCTCTGCGAGATGAGATGACACAGATGCGATTTACCATGTAT 176584
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RESULT 12
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 ACCESSION BC056052
 VERSION BC056052.1 GI:33417123
 KEYWORDS MGC.
 SOURCE Xenopus laevis (African clawed frog)
 ORGANISM Xenopus laevis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 Xenopodinae; Xenopus.

REFERENCE
 AUTHORS Klein,S.L., Strausberg,R.L., Wagner,L., Pontius,J., Clifton,S.W., and Richardson,P.
 TITLE Genetic and genomic tools for Xenopus research: The NIH Xenopus Initiative
 JOURNAL Dev. Dyn. 225 (4), 384-391 (2002)
 MEDLINE 22341132
 PUBMED 12454917
 REFERENCE
 AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marudina,K., Farmer,A.S., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Uedin,T.B., Teohiyuki,S., Carninci,P., Frange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullany,S.U., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., Young,A.C., Shevchenko,Y., Sanchez,A., Whiting,M., Touchman,J.W., Green,E.D., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickinson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalios,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
 TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16999-16903 (2002)
 MEDLINE 22388257
 PUBMED 12477932
 REFERENCE
 AUTHORS Klein,S. and Strausberg,R.
 TITLE Direct Submission
 JOURNAL Submitted (01-AUG-2003) National Institutes of Health, Xenopus Gene Collection (XGC), National Institute of Child Health and Human Development, 6100 Executive Boulevard, Room 4B01, Rockville, MD 20852-7510, USA
 REMARK
 COMMENT NIH-MGC Project
 Contact: XGC help desk
 Email: cgabbs@mail.nih.gov
 Tissue procurement: Dr. Igor Dawid
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLUM)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: http://www.shgc.stanford.edu
 Contact: (Dickson, Mark) mcd@paxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILLUM at: http://image.llnl.gov
 Series: IRAC Plate: 129 Row: 1 Column: 1
 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, similarity but not identity to protein.
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 Gene
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Best Local Similarity 60.5%; Pred. No. 6.4e-56;
Matches 454; Conservative 0; Mismatches 296; Indels 1; Gaps 1;

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QY 317 TTGGATACCTCGAGAAAAGGACAGGATCTGTCTGTGATGTGGAGATCCGGA 376
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RESULT 13
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LOCUS      BD103332
DEFINITION Novel collectin.
ACCESSION BD103332
VERSION    BD103332.1 GI:22648906
KEYWORDS   WO 0181401-A/31
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 813)
            Wakamiya,N., Keshi,H., Otani,K., Sakamoto,T. and Kishi,Y.
            Patent: WO 0181401-A 31 01-NOV-2001;
            FUSO PHARMACEUTICAL INDUSTRIES LTD,NOBUTAKA WAKAMIYA,HIROYUKI
            KESHI, KATSUKI OTANI,TAKASHI SAKAMOTO,YUICHIRO KISHI
COMMENT     OS Homo sapiens (human)
            PN WO 0181401-A/31
            PD 01-NOV-2001
            PF 23-APR-2001 WO 2001JP003468
            PR 21-APR-2000 JP 00P 120358
            PI NOBUTAKA WAKAMIYA,HIROYUKI KESHI,KATSUKI OTANI,TAKASHI PI
            SAKAMOTO,
            YUICHIRO KISHI
            PC C07K14/47,C12N15/12,C12P21/02,A01K67/027,C07K16/18,G01N33/53
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Query Match      29.4%; Score 244.6; DB 6; Length 813;
Best Local Similarity 58.4%; Pred. No. 1.1e-50;
Matches 427; Conservative 0; Mismatches 304; Indels 0; Gaps 0;

QY 101 CTACCGTGAAGTCTGTGTCACACACACAAATTTACAGAGTCCGAGCAATTTGGCAAGCTGGGCCCA 160
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QY 401 GTATTGCCCGGCTCAAGACATCTATGAAGTTTGTCAAGATGTGTAGATGAGGGATTAGG 460
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QY 461 AAATGAGAGAAATTTCTACTACATGTGCGAGAGAGAGAACTACAGGGATCCCTAA 520
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DEFINITION Sequence 356 from patent US 6478825.
ACCESSION AR252616
VERSION AR252616.1 GI:27300524
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1. (bases 1 to 1238)
AUTHORS Winterbottom, J.M., Shimp, L., Boyce, T.M. and Kaes, D.
TITLE Implant, method of making same and use of the implant for the
treatment of bone defects
JOURNAL Patent: US 6478825-A 356 12-NOV-2002;
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Best Local Similarity 58.4%; Pred. No. 1.1e-50;
Matches 427; Conservative 0; Mismatches 304; Indels 0; Gaps 0;

QY 101 CTACCGCTGAAGTCTGTGCCACACACAAATTTCCAGGACCCCAAGAGATGATGGTG 160
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701 GGAATGAGGGGAGAACCCAGCGACCCCTATGTGTCATGAGGACTGTGAGATGCTGAGCT 760
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DEFINITION Sequence 356 from Patent WO0073454.
ACCESSION AX403469
VERSION AX403469.1 GI:21436970
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1. (bases 1 to 1238)
AUTHORS Ashkenazi, A.J., Baker, K.P., Botstein, D., Desnoyers, L., Eaton, D.,
Ferrara, N., Gerber, H., Gerritsen, M., Goddard, A., Godowski, P.,
Grimaldi, C.J., Gurney, A.L., Kljavin, I., Napier, M.A., Pan, J.,
Paoni, N.F., Roy, M., Stewart, T.A., Tumas, D., Watanabe, C.K.,
Williams, P., Wood, W.I. and Zhang, Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0073454-A 356 07-DEC-2000;
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Query Match 29.4%; Score 244.6; DB 6; Length 1238;
Best Local Similarity 58.4%; Pred. No. 1.1e-50;
Matches 427; Conservative 0; Mismatches 304; Indels 0; Gaps 0;

QY 101 CTACCGCTGAAGTCTGTGCCACACAAATTTCCAGGACCCCAAGGAGATGATGGTG 160
DB 149 CTGGCGATGACGCGCTCTGTGTGAGATCCTCGTCCCTCAAAGGGATGCGGGAG 208
QY 161 AAAAAGGAGATCCAGGAGAGGAGGAAAGCATGGCAAAAGTGGGACGCGATGGGCCGAAAG 220
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DB 269 GAGACATGGGGGCAAAAGGACAGAAAGGAGTGTGGGTGCTCATGAAAATTTGGTCCA 328
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 Job time : 3309 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 16:43:17 ; Search time 398 Seconds

(without alignments)
8869.981 Million cell updates/sec

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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1: Geneseqn1980s.*

2: Geneseqn1990s.*

3: Geneseqn2000s.*

4: Geneseqn2001as.*

5: Geneseqn2001bs.*

6: Geneseqn2002s.*

7: Geneseqn2003as.*

8: Geneseqn2003bs.*

9: Geneseqn2003cs.*

10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4	826.2	99.4	1016	4	AAa45974	Human DNA
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8	826.2	99.4	1016	7	ACC87557	Human sec
9	826.2	99.4	1016	7	ACC86943	Human sec
10	826.2	99.4	1016	7	ACD04116	Human sec
11	826.2	99.4	1016	7	ACA69447	CDNA enco
12	826.2	99.4	1016	7	ACA90292	Novel hum
13	826.2	99.4	1016	7	ACC89399	Human sec
14	826.2	99.4	1016	7	ACA98190	Human sec
15	826.2	99.4	1016	7	ACA93832	Human sec
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ALIGNMENTS

RESULT 1

AAx88323

ID AAX88323 standard; CDNA; 1595 BP.

XX AC AAX88323;

XX DT 30-SEP-1999 (first entry)

XX DE Human collectin cDNA.

XX KW Collectin; human; antibacterial; antiviral; treatment; infection; ds.

XX OS Homo sapiens.

XX FH Key

XX CDS Location/Qualifiers

XX FT 6..839

XX FT /*tag= a

XX FT /product= "collectin"

XX PN WO9937767-Al.

XX PD 29-JUL-1999.

XX PF 24-JUL-1998; 98WO-JP003328.

XX PR 23-JAN-1998; 98JP-00011281.

XX PA (FUSO) FUSO PHARM IND LTD.

XX PI Wakamiya N;

XX DR WPI; 1999-458691/38.

XX DR F-PSDB; AAY25518.

XX PT New collectin protein of human origin and DNA encoding it.

XX PS Claim 2; page 39-42; 58pp; Japanese.

XX CC This invention describes the isolation and characterisation of a novel

XX CC human collectin protein and its encoding polynucleotide. The human

XX CC collectin exhibits antibacterial and antiviral activity and can be used

XX CC as an agent for the treatment of human bacterial and viral infections.

XX CC This sequence encodes the novel human collectin

XX SQ Sequence 1595 BP; 444 A; 322 C; 382 G; 447 T; 0 U; 0 Other;

Query Match		100.0%; Score 831; DB 2; Length 1595;
Best Local Similarity		100.0%; Pred. No. 1.4e-242;
Matches 831; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1	ATGAATGGCTTTGGATCTCTGCTTCGAGAAACCAATTTATCTCTCTGCTACTATTCTT 60
Db	6	ATGAATGGCTTTGGATCTCTGCTTCGAGAAACCAATTTATCTCTCTGCTACTATTCTT 65
Qy	61	TTGCAATTCAGATCTGGGCTCTGGATATTGATAGCGCTCTACCGCTGAGTCTGTGCC 120
Db	66	TTGCAATTCAGATCTGGGCTCTGGATATTGATAGCGCTCTACCGCTGAGTCTGTGCC 125
Qy	121	ACACACACATTTCCACGAGACCCCAAGAGAGATGATGTTGAAAGAGATCCAGAGAA 180
Db	126	ACACACACATTTCCACGAGACCCCAAGAGAGATGATGTTGAAAGAGATCCAGAGAA 185
Qy	181	GAGGAAAGCATGCGCAAGTGGGACGATGGGCGGAAAGAAATTAAAGAGAACTGGGT 240
Db	186	GAGGAAAGCATGCGCAAGTGGGACGATGGGCGGAAAGAAATTAAAGAGAACTGGGT 245
Qy	241	GATATGGAGATCGGGCCATATTGGCAAGACTGGGCCCATTTGGGAGAGAGGTGACAA 300
Db	246	GATATGGAGATCGGGCCATATTGGCAAGACTGGGCCCATTTGGGAGAGAGGTGACAA 305
Qy	301	GGGAAAAAGTTTTCCTTGGAAATACCTGGAGAAAAAGGCAAGCAGGTACTGTCTGTAT 360
Db	306	GGGAAAAAGTTTTCCTTGGAAATACCTGGAGAAAAAGGCAAGCAGGTACTGTCTGTAT 365
Qy	361	TGTGAAATACCGGAAATTTTGGCAACTGGATATTAGTATTCCTCGGCTCAAGACA 420
Db	366	TGTGAAATACCGGAAATTTTGGCAACTGGATATTAGTATTCCTCGGCTCAAGACA 425
Qy	421	TCTATGAAATTTGTCAAGATGTGATAGCAGGATTTAGGAAAACTGAAGAGAAATTTCTAC 480
Db	426	TCTATGAAATTTGTCAAGATGTGATAGCAGGATTTAGGAAAACTGAAGAGAAATTTCTAC 485
Qy	481	TACATCGTGCAGAGAGAGAACTACAGGAAATCCCTACCCCACTGCAGGATTCGGGT 540
Db	486	TACATCGTGCAGAGAGAGAACTACAGGAAATCCCTACCCCACTGCAGGATTCGGGT 545
Qy	541	GGAAATGCTAGCATGCCCAAGGATGAAGCTGCCCAACACACTCATCGTCACTATGTTGCC 600
Db	546	GGAAATGCTAGCATGCCCAAGGATGAAGCTGCCCAACACACTCATCGTCACTATGTTGCC 605
Qy	601	AAGATGGCTTTTCGGGCTTCATTTGGCGTGAATGACCTTGAAGAGGAGGACAGTAC 660
Db	606	AAGATGGCTTTTCGGGCTTCATTTGGCGTGAATGACCTTGAAGAGGAGGACAGTAC 665
Qy	661	ATGTTTCAGAGACACACTCCCACTGAGAACTATAGCAACTGGAATGAGGGGAAACCCAGC 720
Db	666	ATGTTTCAGAGACACACTCCCACTGAGAACTATAGCAACTGGAATGAGGGGAAACCCAGC 725
Qy	721	GACCCCTATGTCATGAGACACTGTGTGAGATGCTGAGCTCTGCGAGATGGAATGACACA 780
Db	726	GACCCCTATGTCATGAGACACTGTGTGAGATGCTGAGCTCTGCGAGATGGAATGACACA 785
Qy	781	GAGTGCATCTTACCATGCTACTTTGCTGTGAGTTTCATCAAGAGAAAAAG 831
Db	786	GAGTGCATCTTACCATGCTACTTTGCTGTGAGTTTCATCAAGAGAAAAAG 836

RESULT 2
AAZ33973
ID AAZ33973 standard; cDNA; 1016 BP.
XX
AC AAZ33973;
XX
XX
DT 07-DEC-1999 (first entry)
XX
DE Human PRO702 nucleotide sequence.
XX
KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;

KW	secreted protein; transmembrane protein; ss.
XX	Homo sapiens.
OS	MO9946281-A2.
XX	16-SEP-1999.
XX	08-MAR-1999;
PF	99WO-US005028.
XX	10-MAR-1998;
PR	98US-0077450P.
PR	98US-0077632P.
PR	98US-0077641P.
PR	98US-0077649P.
PR	98US-0077791P.
PR	98US-0078004P.
PR	98US-00040220.
PR	98US-0078886P.
PR	98US-0078910P.
PR	98US-0078936P.
PR	98US-0078939P.
PR	98US-0079294P.
PR	98US-0079656P.
PR	98US-0079663P.
PR	98US-0079664P.
PR	98US-0079689P.
PR	98US-0079728P.
PR	98US-0079786P.
PR	98US-0079920P.
PR	98US-0079923P.
PR	98US-0080105P.
PR	98US-0080107P.
PR	98US-0080165P.
PR	98US-0080194P.
PR	98US-0080327P.
PR	98US-0080328P.
PR	98US-0080333P.
PR	98US-0080334P.
PR	98US-0081049P.
PR	98US-0081070P.
PR	98US-0081071P.
PR	98US-0081195P.
PR	98US-0081203P.
PR	98US-0081229P.
PR	98US-0081817P.
PR	98US-0081838P.
PR	98US-0081952P.
PR	98US-0081955P.
PR	98US-0082568P.
PR	98US-0082569P.
PR	98US-0082700P.
PR	98US-0082704P.
PR	98US-0082804P.
PR	98US-0082767P.
PR	98US-0082796P.
PR	98US-0083336P.
PR	98US-0083322P.
PR	98US-0083392P.
PR	98US-0083495P.
PR	98US-0083496P.
PR	98US-0083499P.
PR	98US-0083500P.
PR	98US-0083545P.
PR	98US-0083554P.
PR	98US-0083558P.
PR	98US-0083559P.
PR	98US-0083742P.
PR	98US-0084366P.
PR	98US-0084414P.
PR	98US-0084598P.
PR	98US-0084600P.
PR	98US-0084627P.

PR 07-MAY-1998; 98US-0084637P.
PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
PR 07-MAY-1998; 98US-0084643P.
PR 13-MAY-1998; 98US-0085323P.
PR 13-MAY-1998; 98US-0085338P.
PR 13-MAY-1998; 98US-0085339P.
PR 15-MAY-1998; 98US-0085573P.
PR 15-MAY-1998; 98US-0085579P.
PR 15-MAY-1998; 98US-0085580P.
PR 15-MAY-1998; 98US-0085582P.
PR 15-MAY-1998; 98US-0085689P.
PR 15-MAY-1998; 98US-0085697P.
PR 15-MAY-1998; 98US-0085700P.
PR 15-MAY-1998; 98US-0085704P.
PR 18-MAY-1998; 98US-0086023P.
PR 22-MAY-1998; 98US-0086392P.
PR 22-MAY-1998; 98US-0086414P.
PR 22-MAY-1998; 98US-0086430P.
PR 22-MAY-1998; 98US-0086486P.
PR 28-MAY-1998; 98US-0087098P.
PR 28-MAY-1998; 98US-0087106P.
PR 28-MAY-1998; 98US-0087208P.
PR 30-JUL-1998; 98US-0094651P.
PR 11-SEP-1998; 98US-0100038P.
XX (GETH) GENENTECH INC.
XX
XX Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
PI
XX MPI; 1999-551358/46.
XX P-PSDB; AAY41698.
XX
XX New secreted and transmembrane polypeptides and their polynucleotides,
XX useful for treating blood coagulation disorders, cancers and cellular
XX adhesion disorders.
XX
XX Claim 2; Fig 36; 530pp; English.
XX
XX The present invention describes secreted and transmembrane polypeptides
XX and their polynucleotides. The nucleotide sequences are useful as sources
XX of probes, primers, for chromosome mapping, and for generation of
XX antisense sequences. They can also be used to create transgenic animals.
XX The proteins can be used to treat a variety of diseases and disorders,
XX depending on their function. Diseases that may be treated include blood
XX coagulation disorders, cancers and cellular adhesion disorders. They may
XX also be used to raise antibodies. AA33891 to AA34338, and AAY41685 to
XX AA41774 represent polynucleotide and polypeptide sequence given in the
XX exemplification of the present invention
XX
XX Sequence 1016 BP; 312 A; 197 C; 261 G; 246 T; 0 U; 0 Other;
XX
XX Query Match 99.4%; Score 826.2; DB 2; Length 1016;
XX Best Local Similarity 99.6%; Pred. No. 3.2e-241;
XX Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1 ATGAATGCTTGGATCTTCTGCTTCCAGAGAAACCAATTTATCTCTCTGCTACTATTCTT 60
XX 22 ATGAATGCTTGGATCTTCTGCTTCCAGAGAAACCAATTTATCTCTCTGCTACTATTCTT 81
XX
XX 61 TTGCAAAATTCAGATCTGGGTCTGGATATTGATAGCGCTCTACCGCTGAACTCTGTGCC 120
XX 82 TTGCAAAATTCAGATCTGGGTCTGGATATTGATAGCGCTCTACCGCTGAACTCTGTGCC 141
XX
XX 121 ACACACAAATTTCCACAGACCCCAAGAGAGATGATGGTGAAGAAAGAGATCCAGAGAA 180
XX 142 ACACACAAATTTCCACAGACCCCAAGAGAGATGATGGTGAAGAAAGAGATCCAGAGAA 201
XX
XX 181 GAGGGAAGCATGCGCAAGTGGAGCATGGGCCGCAAGAGAAATTAAGGAGAACTGGGT 240
XX 202 GAGGGAAGCATGCGCAAGTGGAGCATGGGCCGCAAGAGAAATTAAGGAGAACTGGGT 261
XX
XX 241 GATATGGAGATCGGGGCAATATTGGCAAGCATGGGCCCACTGGGAGAGAGGTCACAAA 300

Db 262 GATATGGAGATCAGGGCAATATTGCAAGACTGGGCCCATTTGGGAAGAGGGTGACAAA 321
Qy 301 GGGGAAAAAGTTTGTCTTGAATACCTGGAGAAAAAGGCAAAAGCAGGTACTCTCTGTGAT 360
Db 322 GGGGAAAAAGTTTGTCTTGAATACCTGGAGAAAAAGGCAAAAGCAGGTACTCTCTGTGAT 381
Qy 361 TGTGGAGATACCGGAAATTTGTTGACAACTGGATATTAGTATTGCCCGGCTCAAGACA 420
Db 382 TGTGGAGATACCGGAAATTTGTTGACAACTGGATATTAGTATTGCCCGGCTCAAGACA 441
Qy 421 TCTATGAAGTTTCTCAAGAAATGTGATAGCAGGATTTAGGAAACTGAAGAGAAATTTCTAC 480
Db 442 TCTATGAAGTTTCTCAAGAAATGTGATAGCAGGATTTAGGAAACTGAAGAGAAATTTCTAC 501
Qy 481 TACATGTCGAGGAGAGAACTACACGGGATCCCTAACCCACTGACGAGGATTCGGGGT 540
Db 502 TACATGTCGAGGAGAGAACTACACGGGATCCCTAACCCACTGACGAGGATTCGGGGT 561
Qy 541 GGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACAACACTCATCGCTGACTATTTGCC 600
Db 562 GGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACAACACTCATCGCTGACTATTTGCC 621
Qy 601 AAGATGGCTTCTTTTCGGGTGTTTCATTCGCGTGAATGACCTTGAAGGGGAGGACAGTAC 660
Db 622 AAGATGGCTTCTTTTCGGGTGTTTCATTCGCGTGAATGACCTTGAAGGGGAGGACAGTAC 681
Qy 661 ATGTTTCCACAGACAACTCCACTGCAGAACTATAGCACTGGAATGAGGGGGAACCCAGC 720
Db 682 ATGTTTCCACAGACAACTCCACTGCAGAACTATAGCACTGGAATGAGGGGGAACCCAGC 741
Qy 721 GACCCCTATGCTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACA 780
Db 742 GACCCCTATGCTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACA 801
Qy 781 GAGTGCCATCTTACCATGTACTTGTCTGTGAGTTTCATCAAGAAAGAAAAG 831
Db 802 GAGTGCCATCTTACCATGTACTTGTCTGTGAGTTTCATCAAGAAAGAAAAG 852

RESULT 3
AAC78480
ID AAC78480 standard; cDNA; 1016 BP.
XX AAC78480;
AC AAC78480;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human PR0702 (UNQ366) nucleotide sequence SEQ ID NO:96.
XX
XX Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;
XX expressed sequence tag; detection; cancer; ss.
XX
OS Homo sapiens.
XX
XX WO200053756-A2.
XX
XX 14-SEP-2000.
XX
XX 18-FEB-2000; 2000HO-US004341.
XX
XX 08-MAR-1999; 99WO-US005028.
XX 12-MAR-1999; 99US-0123957P.
XX 29-MAR-1999; 99US-0126773P.
XX 21-APR-1999; 99US-0130232P.
XX 28-APR-1999; 99US-0131445P.
XX 14-MAY-1999; 99US-0134287P.
XX 23-JUN-1999; 99US-0141037P.
XX 26-JUL-1999; 99US-0145698P.
XX 30-NOV-1999; 99WO-US028313.
XX 02-DEC-1999; 99WO-US028551.
XX 02-DEC-1999; 99WO-US028565.

PR 16-DEC-1999; 99WO-US030095.
 PR 30-DEC-1999; 99WO-US031243.
 PR 30-DEC-1999; 99WO-US031274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 06-JAN-2000; 2000WO-US000376.
 XX (GETH) GENENTECH INC.
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
 PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
 PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy WA, Shelton DL;
 PI Stewart TA, Tunas D, Williams PM, Wood WI;
 XX WPI; 2000-611443/58.
 DR P-PSDB; AAB44254.
 XX
 XX Novel PRO polypeptides and polynucleotides used in detection methods, to
 PT target bioactive molecules to specific cells, and to modulate cellular
 PT activities.
 XX
 PS Claim 2; Fig 36; 636pp; English.
 XX
 CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence
 CC tag) sequences which encode secreted or transmembrane PRO polypeptides.
 CC The PRO polynucleotides and polypeptides have cytostatic activity. The
 CC polynucleotides and polypeptides can be used for detecting the presence
 CC of PRO polypeptides in samples, for linking bioactive molecules to cells
 CC and for modulating biological activities of cells, using the polypeptides
 CC for specific targeting. The polypeptide targeting can be used to kill the
 CC target cells, e.g. for the treatment of cancers. The polypeptide pairs
 CC provide specific targeting of bioactive molecules to cells. AAC78600 to
 CC AAC78987 represent PCR primers and probes used in the isolation of the
 CC PRO polynucleotide sequences
 XX
 SQ Sequence 1016 BP; 312 A; 197 C; 261 G; 246 T; 0 U; 0 Other;
 Query Match 99.4%; Score 926.2; DB 3; Length 1016;
 Best Local Similarity 99.6%; Pred. No. 3.2e-241;
 Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 1 ATGATGCTTGGATCCTCTCGAGAAACCAATTTATCTCTGCTGCTATTTCTT 60
 22 ATGATGCTTGGATCCTCTCGAGAAACCAATTTATCTCTGCTGCTATTTCTT 81
 61 TTGCAAAATCAGAGTCTGGGTCCTGGATTTGATAGCGCTCTACCGCTGAAGTCTGTGCC 120
 82 TTGCAAAATCAGAGTCTGGGTCCTGGATTTGATAGCGCTCTACCGCTGAAGTCTGTGCC 141
 121 ACACACAAATTTCCAGGACCCCAAGAGAGATGATGGTGAAGAGAGATCCAGAGAA 180
 142 ACACACAAATTTCCAGGACCCCAAGAGAGATGATGGTGAAGAGAGATCCAGAGAA 201
 181 GAGGGAAGAGATGGAAGTGGGACGATGGGCGGGAAGGAATTAAGAGAGAACTGGGT 240
 202 GAGGGAAGAGATGGAAGTGGGACGATGGGCGGGAAGGAATTAAGAGAGAACTGGGT 261
 241 GATATGGAGATCGGGGCAATTTGGAGAGCTGGGCGGCAATGGGAAGAGAGGTGACAA 300
 262 GATATGGAGATCGGGGCAATTTGGAGAGCTGGGCGGCAATGGGAAGAGAGGTGACAA 321
 301 GGGGAAAAGGTTTCTTGGGAATACCTGGGAAAAGGCAAGCAGTACTGTCTGTGAT 360
 322 GGGGAAAAGGTTTCTTGGGAATACCTGGGAAAAGGCAAGCAGTACTGTCTGTGAT 381
 361 TGTGGAAGATCCGGAATTTGTTGGCAACTGATATAGTATGTCGGGCTCAAGACA 420
 382 TGTGGAAGATCCGGAATTTGTTGGCAACTGATATAGTATGTCGGGCTCAAGACA 441
 421 TCTATGAATTTGTCAGAAATGTCATAGCAGGATTTAGGGAATTAAGAGAAATTTCTAC 480
 442 TCTATGAATTTGTCAGAAATGTCATAGCAGGATTTAGGGAATTAAGAGAAATTTCTAC 501

QY 481 TACATCGTCGAGAGAGAAAGAACTACAGGGAAATCCCTAACCCACTGCAGGATTCGGGGT 540
 DB 502 TACATCGTCGAGAGAGAGAAAGAACTACAGGGAAATCCCTAACCCACTGCAGGATTCGGGGT 561
 QY 541 GGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACACACTCATCGCTGACTATGTTGCC 600
 DB 562 GGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACACACTCATCGCTGACTATGTTGCC 621
 QY 601 AAGAGTGGCTCTTTTCGGGTGTTCAATGCGGTGAATGACCTTGAAGGGAGGACAGTAC 660
 DB 622 AAGAGTGGCTCTTTTCGGGTGTTCAATGCGGTGAATGACCTTGAAGGGAGGACAGTAC 681
 QY 661 ATGTTTCAACAGACAACTCCACTGCGAGACTATGCACTGGAATGAGGGGAAACCCAGC 720
 DB 682 ATGTTTCAACAGACAACTCCACTGCGAGACTATGCACTGGAATGAGGGGAAACCCAGC 741
 QY 721 GACCCCTATGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACA 780
 DB 742 GACCCCTATGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACA 801
 QY 781 GAGTGGCACTTTACCATGCTACTTTGCTGTGAGTTTCATCAAGAGAAAAAG 831
 DB 802 GAGTGGCACTTTACCATGCTACTTTGCTGTGAGTTTCATCAAGAGAAAAAG 852
 RESULT 4
 AAS45974
 ID AAS45974 standard; cDNA; 1016 BP.
 AC AAS45974;
 XX
 DT 18-DEC-2001 (first entry)
 DE Human DNA encoding PRO polypeptide sequence #50.
 XX
 KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;
 KW dog; cat; pig; goat; rabbit; tumour necrosis factor; alpha; TNF-alpha; colon;
 KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
 KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
 KW PCR primer.
 XX
 OS Homo sapiens.
 XX
 FN WO200168848-A2.
 XX
 PD 20-SEP-2001.
 XX
 PF 28-FEB-2001; 2001WO-US006520.
 XX
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 03-MAR-2000; 2000US-0187202P.
 PR 06-MAR-2000; 2000US-0186968P.
 PR 14-MAR-2000; 2000US-0189320P.
 PR 14-MAR-2000; 2000US-0189328P.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 21-MAR-2000; 2000US-0190828P.
 PR 21-MAR-2000; 2000US-0191007P.
 PR 21-MAR-2000; 2000US-0191048P.
 PR 21-MAR-2000; 2000US-0191314P.
 PR 28-MAR-2000; 2000US-0192655P.
 PR 29-MAR-2000; 2000US-0193032P.
 PR 29-MAR-2000; 2000US-0193053P.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 04-APR-2000; 2000US-0194449P.
 PR 04-APR-2000; 2000US-0194647P.
 PR 11-APR-2000; 2000US-0195975P.
 PR 11-APR-2000; 2000US-0196000P.
 PR 11-APR-2000; 2000US-0196187P.
 PR 11-APR-2000; 2000US-0196690P.
 PR 11-APR-2000; 2000US-0196820P.
 PR 18-APR-2000; 2000US-0198121P.

PR 18-APR-2000; 2000US-0198585P.
PR 23-APR-2000; 2000US-0199397P.
PR 25-APR-2000; 2000US-0199550P.
PR 25-APR-2000; 2000US-0199654P.
PR 03-MAY-2000; 2000US-0201516P.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 05-JUN-2000; 2000US-0209832P.
PR 28-JUL-2000; 2000WO-US020710.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032278.
PR 20-DEC-2000; 2000WO-US034956.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI: 2001-602746/68.
DR P-PSDB; AAU29073.
XX
XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT presence of tumors, such as prostate and breast tumors, in mammals and to
PT screen for modulators of the compounds.
XX
XX Claim 2; Fig 99; 774pp; English.
XX
CC Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR
CC primers for PRO polypeptides of the invention. The sequences of the
CC inverting can be used to detect the presence of a tumour in a mammal by
CC comparing the level of expression of a PRO polypeptide in a test sample
CC of cells from the animal and a control sample of normal cells, whereby a
CC higher level of expression in the test sample indicates the presence of a
CC tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,
CC pigs, goats and rabbits but are preferably human. The polypeptides can be
CC used to stimulate tumour necrosis factor (TNF) alpha release from human
CC blood, when contacted with it. A specific polypeptide can be used to
CC stimulate the proliferation or differentiation of chondrocyte cells. The
CC PRO proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders
XX
SQ Sequence 1016 BP; 312 A; 197 C; 261 G; 246 T; 0 U; 0 Other;
Query Match 99.4%; Score 826.2; DB 4; Length 1016;
Best Local Similarity 99.6%; Pred. No. 3.2e-241;
Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
2Y 1 ATGAATGCTTTGGCATCTTGCTTCGAGAAACCAATTATCTCTGCTGCTACTATTCTT 60
DB 22 ATGAATGCTTTGGCATCTTGCTTCGAGAAACCAATTATCTCTGCTGCTACTATTCTT 81
2Y 61 TTGCAATTCAGATCTGGGTCTGGATTTGATAGCGCTCTACCCCTGAAGTCTGTGCC 120
DB 82 TTGCAATTCAGATCTGGGTCTGGATTTGATAGCGCTCTACCCCTGAAGTCTGTGCC 141
2Y 121 ACACACAAATTCACACAGACCCCAAGAGAGATGATGGTGAAGAGAGATCCAGAGAA 180
DB 142 ACACACAAATTCACACAGACCCCAAGAGAGATGATGGTGAAGAGAGATCCAGAGAA 201
2Y 181 GAGGGAAGAGATGCAAGTGGGACGATCGTGGGCCGGAAGAAATTAAGAGAACTGGGT 240
DB 202 GAGGGAAGAGATGCAAGTGGGACGATCGTGGGCCGGAAGAAATTAAGAGAACTGGGT 261
2Y 241 GATATGGAGATCGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGAGGTGACAAA 300
DB 262 GATATGGAGATCGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGAGGTGACAAA 321

QY 301 GGGGAAAAGGTTTGGTGGAAATACCTGGAGAAAAAGGCAAGCACTGTCTGTGTAT 360
DB 322 GGGGAAAAGGTTTGGTGGAAATACCTGGAGAAAAAGGCAAGCACTGTCTGTGTAT 381
QY 361 TGTGGAAGATACCGGAAATTTGTGGCAACTGGATATTAGTATTGCCCGCTCAGACA 420
DB 382 TGTGGAAGATACCGGAAATTTGTGGCAACTGGATATTAGTATTGCCCGCTCAGACA 441
QY 421 TCTATGAAGTTTGTCAAGAAATGTGATAGCAGGGAATTAGGGAACCTCAAGAGAAATCTTAC 480
DB 442 TCTATGAAGTTTGTCAAGAAATGTGATAGCAGGGAATTAGGGAACCTCAAGAGAAATCTTAC 501
QY 481 TACATCTGTCAGGAGAGAGAACTACAGGGAATCCCTAACCACTGACAGGATTCGGGT 540
DB 502 TACATCTGTCAGGAGAGAGAACTACAGGGAATCCCTAACCACTGACAGGATTCGGGT 561
QY 541 GGAATGCTAGCTAGCCCAAGGATGAAGCTGCCCAACACACTCATCTGCTGCTATGTGCC 600
DB 562 GGAATGCTAGCTAGCCCAAGGATGAAGCTGCCCAACACACTCATCTGCTGCTATGTGCC 621
QY 601 AAGAGTGGCTTCTTCGGGTGTTTCATTGGGTGATGACCTTGAAGAGGAGGACAGTAC 660
DB 622 AAGAGTGGCTTCTTCGGGTGTTTCATTGGGTGATGACCTTGAAGAGGAGGACAGTAC 681
QY 661 ATGTTTACAGACAACACTCCACTGCAGAACTATAGCAACTGCAATGAGGGGAAACCCAGC 720
DB 682 ATGTTTACAGACAACACTCCACTGCAGAACTATAGCAACTGCAATGAGGGGAAACCCAGC 741
QY 721 GACCCCTATGCTATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACA 780
DB 742 GACCCCTATGCTATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACA 801
QY 781 GAGTGCCATCTTACCATTGCTTGTGAGTTTCAATCAAGAAAGAAAAG 831
DB 802 GAGTGCCATCTTACCATTGCTTGTGAGTTTCAATCAAGAAAGAAAAG 852
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ID ABX78577 standard; cDNA; 1016 BP.
AC ABX78577;
XX 15-APR-2003 (first entry)
XX Human PRO polynucleotide #50.
XX Human; PRO; gene; ss; cytostatic; tumour; cancer; breast; lung; stomach;
XX liver; dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;
XX antibody-dependent enzyme mediated prodrug therapy.
XX Homo sapiens.
XX US2003027272-A1.
XX 06-FEB-2003.
XX 21-JUN-2002; 2002US-00176492.
XX 18-SEP-1997; 97US-0059263P.
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Query Match          99.4%; Score 826.2; DB 7; Length 1016;
Best Local Similarity 99.6%; Pred No. 3.2e-241;
Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 82 TTGCAAAATTCAGAGTCTGGTCTTGATATTTGATAGCCGCTCTACCGCTGAAGTCTGTGCC 141
QY 121 ACACACAAATTTACAGGACCCAAAGAGATGATGTGTAAGAGAGATGCCAGGAGAA 180
DB 142 ACACACAAATTTACAGGACCCAAAGAGATGATGTGTAAGAGAGATGCCAGGAGAA 201
QY 181 GAGGGAAGCATGGCAAGTGGGAGCGCATGGGCGGAAGGAATTAAGGAGACTGGT 240
DB 202 GAGGGAAGCATGGCAAGTGGGAGCGCATGGGCGGAAGGAATTAAGGAGAACTGGT 261
QY 241 GATATGGGAGATCGGGGCAATATTTGGCAAGACTGGGCCCATTTGGGAAGAGGGTGACAAA 300
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QY 301 GGGGAAAAGGTTTCTTGGATATCTGGAGAAAGCAAGCAGGTACTGTCTGTGAT 360
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QY 361 TGTGGAAGATACCGGAAATTTCTTGGCAACTGGATATTAGTATTTGCCCGGCTCAAGACA 420
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QY 781 GAGTGGCCATCTTACCATGCTACTTTCTGTCTGTGAGTTCATCAAGAGAAAAAG 831
DB 802 GAGTGGCCATCTTACCATGCTACTTTCTGTCTGTGAGTTCATCAAGAGAAAAAG 852

RESULT 6
ACA75549
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AC ACA75549;
XX
DT 07-JUL-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO702 cDNA.
XX
KW Human; secreted and transmembrane protein; PRO; gene therapy;
KW tumour necrosis factor-alpha release; TNF-alpha release;
KW chondrocyte proliferation; chondrocyte differentiation; tumour;
KW adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003032127-A1.
XX
PD 13-FEB-2003.
XX
PF 26-JUN-2002; 2002US-00183012.
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PR 17-OCT-1997; 97US-0062250P.
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Query Match 99.4%; Score 826.2; DB 7; Length 1016;
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QY	181	GAGGAAAGATCGGCAAAAGTGGGACGCTAGGGGCGGAAAGGAAATTAAGGAGAACTGGT	240	PR	17-OCT-1997; 97US-0082250P.
Db	202	GAGGAAAGATCGGCAAAAGTGGGACGCTAGGGGCGGAAAGGAAATTAAGGAGAACTGGT	261	PR	21-OCT-1997; 97US-0083486P.
QY	241	GATATGGGAGATCGGGGCAATATTCGCAAGACTGGGCCCATTCGGAAGAGAGGTGACAA	300	PR	24-OCT-1997; 97US-0083120P.
Db	262	GATATGGGAGATCGGGGCAATATTCGCAAGACTGGGCCCATTCGGAAGAGAGGTGACAA	321	PR	28-OCT-1997; 97US-0063540P.
QY	301	GGGAAAAAGGTTTCTTGGATACCTCGAGAAAAAGGCAAGCAGTACTGTCTGTGAT	360	PR	28-OCT-1997; 97US-0063541P.
Db	322	GGGAAAAAGGTTTCTTGGATACCTCGAGAAAAAGGCAAGCAGTACTGTCTGTGAT	381	PR	28-OCT-1997; 97US-0063544P.
QY	361	TCGTGAAGATACCGGAAATTTTGGACAACTGGATATAGTATTCGCCGCTCAGACA	420	PR	29-OCT-1997; 97US-0083584P.
Db	382	TCGTGAAGATACCGGAAATTTTGGACAACTGGATATAGTATTCGCCGCTCAGACA	441	PR	31-OCT-1997; 97US-0083734P.
QY	421	TCTATGAAGTTTGTCAAGAATCTGTAGCAGGATTTAGGGAAACTGAAGAGAAATTTCTAC	480	PR	13-NOV-1997; 97US-0065311P.
Db	442	TCTATGAAGTTTGTCAAGAATCTGTAGCAGGATTTAGGGAAACTGAAGAGAAATTTCTAC	501	PR	21-NOV-1997; 97US-0066120P.
QY	481	TACATCGTCAGGAGAGAGAACTACAGGGAATCCCTAACCCACTCGAGGATTCGGGGT	540	PR	24-NOV-1997; 97US-0066466P.
Db	502	TACATCGTCAGGAGAGAGAACTACAGGGAATCCCTAACCCACTCGAGGATTCGGGGT	561	PR	11-DEC-1997; 97US-0089335P.
QY	541	GGAATGCTAGGATCCCAAGAGTGAAGCTGCCAACACACTCATCGCTGACTATGTTGCC	600	PR	12-DEC-1997; 97US-0069425P.
Db	562	GGAATGCTAGGATCCCAAGAGTGAAGCTGCCAACACACTCATCGCTGACTATGTTGCC	621	PR	18-DEC-1997; 97US-0068017P.
QY	601	AGAGTGGCTTTTTCGGGTGTTCAATGGCTGTGAATGACCTTGAAGAGGAGCAAGTAC	660	PR	10-MAR-1998; 98US-0077450P.
Db	622	AGAGTGGCTTTTTCGGGTGTTCAATGGCTGTGAATGACCTTGAAGAGGAGCAAGTAC	681	PR	11-MAR-1998; 98US-0077649P.
QY	661	ATGTTTCACAGACACACTCCACTGCAGAACTATAGCACTGGAATGAGGGGAAACCCAGC	720	PR	20-MAR-1998; 98US-0078866P.
Db	682	ATGTTTCACAGACACACTCCACTGCAGAACTATAGCACTGGAATGAGGGGAAACCCAGC	741	PR	20-MAR-1998; 98US-0078939P.
QY	721	GACCCCTATGTTTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACA	780	PR	27-MAR-1998; 98US-0079664P.
Db	742	GACCCCTATGTTTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACA	801	PR	27-MAR-1998; 98US-0079786P.
QY	781	GAGTCCCATCTTACCATGTTCTGTGAGTTCTATCAAGAGAAAG 831		PR	31-MAR-1998; 98US-0080107P.
Db	802	GAGTCCCATCTTACCATGTTCTGTGAGTTCTATCAAGAGAAAG 852		PR	31-MAR-1998; 98US-0080194P.
RESULT 7					01-APR-1998; 98US-0080327P.
ACA71029					01-APR-1998; 98US-0080333P.
XX	AC	ACA71029 standard; cDNA; 1016 BP.		PR	08-APR-1998; 98US-0081049P.
XX	AC	ACA71029;		PR	08-APR-1998; 98US-0081195P.
XX	DT	02-AUG-2003 (first entry)		PR	15-APR-1998; 98US-0081838P.
XX	DE	Human secreted/transmembrane protein (PRO) cDNA #50.		PR	21-APR-1998; 98US-0082568P.
XX	KW	Human; gene; ss; secreted and transmembrane protein; PRO; TNF-alpha;		PR	21-APR-1998; 98US-0082569P.
XX	KW	tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;		PR	22-APR-1998; 98US-0082704P.
XX	OS	tissue typing.		PR	28-APR-1998; 98US-0083322P.
XX	OS	Homo sapiens.		PR	29-APR-1998; 98US-0083495P.
XX	PN	US2003032112-A1.		PR	29-APR-1998; 98US-0083499P.
XX	XX			PR	05-MAY-1998; 98US-0083559P.
				PR	06-MAY-1998; 98US-0084366P.
				PR	07-MAY-1998; 98US-0084414P.
				PR	07-MAY-1998; 98US-0084640P.
				PR	15-MAY-1998; 98US-0085579P.
				PR	15-MAY-1998; 98US-0085580P.
				PR	15-MAY-1998; 98US-0085582P.
				PR	18-MAY-1998; 98US-0086023P.
				PR	22-MAY-1998; 98US-0086392P.
				PR	28-MAY-1998; 98US-0086486P.
				PR	28-MAY-1998; 98US-0087098P.
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				PR	04-JUN-1998; 98US-0088029P.
				PR	04-JUN-1998; 98US-0088033P.
				PR	04-JUN-1998; 98US-0088326P.
				PR	05-JUN-1998; 98US-0088367P.
				PR	05-JUN-1998; 98US-0088820P.

PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088722P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088811P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088825P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088863P.
PR 11-JUN-1998; 98US-0088876P.
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PR 12-JUN-1998; 98US-0089105P.
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PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089538P.
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PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089653P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
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PR 24-JUN-1998; 98US-0090435P.
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PR 24-JUN-1998; 98US-0090461P.
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PR 24-JUN-1998; 98US-0090540P.
PR 25-JUN-1998; 98US-0090676P.
PR 25-JUN-1998; 98US-0090678P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090690P.
PR 25-JUN-1998; 98US-0090693P.
PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-00105413.
PR 26-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090863P.
PR 26-JUN-1998; 98US-0091010P.
PR 01-JUL-1998; 98US-0091359P.
PR 01-JUL-1998; 98US-0091544P.
PR 02-JUL-1998; 98US-0091478P.
PR 02-JUL-1998; 98US-0091486P.
PR 02-JUL-1998; 98US-0091626P.
PR 02-JUL-1998; 98US-0091628P.
PR 02-JUL-1998; 98US-0091632P.
PR 24-JUL-1998; 98US-0094008P.
PR 04-AUG-1998; 98US-0095282P.
PR 10-AUG-1998; 98US-0095998P.
PR 10-AUG-1998; 98US-0096012P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
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PR 17-AUG-1998; 98US-0096891P.
PR 17-AUG-1998; 98US-0096897P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0097022P.
PR 26-AUG-1998; 98US-0097952P.
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PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0098014P.
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099602P.

PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099812P.
PR 15-SEP-1998; 98US-0100388P.
PR 16-SEP-1998; 98US-0100622P.
PR 16-SEP-1998; 98US-0100642P.
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PR 16-SEP-1998; 98US-0100683P.
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PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100849P.
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PR 18-SEP-1998; 98US-0101068P.
PR 23-SEP-1998; 98US-0101471P.
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PR 23-SEP-1998; 98US-0101477P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101739P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101922P.
PR 25-SEP-1998; 98US-0101786P.
PR 29-SEP-1998; 98US-0102207P.
PR 29-SEP-1998; 98US-0102240P.
PR 29-SEP-1998; 98US-0102330P.
PR 29-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.
PR 02-OCT-1998; 98US-0102965P.
PR 06-OCT-1998; 98US-0103258P.
PR 06-OCT-1998; 98US-0103449P.
PR 07-OCT-1998; 98US-00168978.

Query Match 99.4%; Score 826.2; DB 7; Length 1016;
Best Local Similarity 99.6%; Pred. No. 3.2e-241;
Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGAATGGCTTTGCTTCCTTCTCGAAGAACCAATTTATCTCTCTGGTACTATTTCTT 60
DB 22 ATGAATGGCTTTGCTTCCTTCTCGAAGAACCAATTTATCTCTCTGGTACTATTTCTT 81
QY 61 TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGCTCTACCGCTGAAGTCTGTGCC 120
DB 82 TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGCTCTACCGCTGAAGTCTGTGCC 141
QY 121 ACACACAAATTTTCACAGGACCCAAAGAGATGATGGTGAAGAGGAGATCCAGAGAA 180
DB 142 ACACACAAATTTTCACAGGACCCAAAGAGATGATGGTGAAGAGGAGATCCAGAGAA 201
QY 181 GAGGAAAGCATGGCAAGATGGGACCGATGGGGCCGAAAGGAATTAAGAGAACTGGGT 240
DB 202 GAGGAAAGCATGGCAAGATGGGACCGATGGGGCCGAAAGGAATTAAGAGAACTGGGT 261
QY 241 GATATGGGATCGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGAGGTCACAAA 300
DB 262 GATATGGGATCGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGAGGTCACAAA 321
QY 301 GGGGAAAAGGTTTGTGGATACCTGGAGAAAAGGCAAGCAGGACTCTGTGTGTAT 360
DB 322 GGGGAAAAGGTTTGTGGATACCTGGAGAAAAGGCAAGCAGGACTCTGTGTGTAT 381
QY 361 TGTGGAAGATACCGGAATTTGTGGCAACTGGATATTAGTATTTGCCCGGTCAAGACA 420
DB 382 TGTGGAAGATACCGGAATTTGTGGCAACTGGATATTAGTATTTGCCCGGTCAAGACA 441
QY 421 TCTATGAAGTTTGTCAAGATGTGATGAGGAGATTAGGGAACCTGAAGAGAAATTCAC 480

Db	442	TCATGAGTTGTCAGAAATGTCATGACGAGGAAATAGGAAACTGAGAGAAATTCCTAC	501	PR	18-DEC-1997;	97US-0068017P.
Qy	481	TACATCGTCGAGGAGAGAACTACAGGAAATCCCTAACCCACTGCGAGATTGCGGGT	540	PR	10-MAR-1998;	98US-0077450P.
Db	502	TACATCGTCGAGGAGAGAACTACAGGAAATCCCTAACCCACTGCGAGATTGCGGGT	561	PR	11-MAR-1998;	98US-0077632P.
Qy	541	GGATGCTAGCCATGCCCAAGGATGAGCTGCCCAACACTCATCGCTACTATGTTGCC	600	PR	20-MAR-1998;	98US-0077886P.
Db	562	GGATGCTAGCCATGCCCAAGGATGAGCTGCCCAACACTCATCGCTACTATGTTGCC	621	PR	20-MAR-1998;	98US-0078939P.
Qy	601	AAGAGTGCTCTTTTCGGGTGTTTCATTGGGGTGAATGACCTTCAAAAGGAGGACAGTAC	660	PR	27-MAR-1998;	98US-0079664P.
Db	622	AAGAGTGCTCTTTTCGGGTGTTTCATTGGGGTGAATGACCTTCAAAAGGAGGACAGTAC	681	PR	27-MAR-1998;	98US-0079786P.
Qy	661	ATGTTTCACAGACACTCCCACTCAGACTAGCACTAGCACTGGAATGAGGGGAAACCCAGC	720	PR	31-MAR-1998;	98US-0080107P.
Db	682	ATGTTTCACAGACACTCCCACTCAGACTAGCACTAGCACTGGAATGAGGGGAAACCCAGC	741	PR	31-MAR-1998;	98US-0080194P.
Qy	721	GACCCCTATGCTATGAGGACTGTGGAGATGCTGAGCTCTGCGAGATGGAATGACACA	780	PR	01-APR-1998;	98US-0080327P.
Db	742	GACCCCTATGCTATGAGGACTGTGGAGATGCTGAGCTCTGCGAGATGGAATGACACA	801	PR	01-APR-1998;	98US-0080333P.
Qy	781	GAGTGCATCTTACATGACTGTTGCTGTTGAGTTCAATCAAGAAAGAAAG	831	PR	08-APR-1998;	98US-0081049P.
Db	802	GAGTGCATCTTACATGACTGTTGCTGTTGAGTTCAATCAAGAAAGAAAG	852	PR	08-APR-1998;	98US-0081070P.
RESULT 8						
AC87557	AC87557 standard; cDNA; 1016 BP.					
XX	AC	AC87557;				
XX	DT	05-AUG-2003 (first entry)				
XX	DE	Human secreted polypeptide PRO702-encoding cDNA, SEQ ID NO:99.				
KW	KW	Human; PRO; secreted protein; transmembrane protein;				
KW	KW	extracellular domain; tumour necrosis factor-alpha; TNF-alpha;				
KW	KW	chondrocyte; proliferation; differentiation; cartilage disorder;				
KW	KW	bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;				
KW	KW	adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;				
KW	KW	liver; drug screening; transgenic animal; genetic analysis;				
KW	KW	antiarthritic; vulnery; gene therapy; gene; ss.				
CS	XX	Homo sapiens.				
PN	XX	US2003027278-A1.				
XX	PD	06-FEB-2003.				
XX	PF	21-JUN-2002; 2002US-00176987.				
XX	PR	18-SEP-1997; 97US-0059263P.				
PR	PR	18-SEP-1997; 97US-0059266P.				
PR	PR	17-OCT-1997; 97US-0062250P.				
PR	PR	21-OCT-1997; 97US-0063486P.				
PR	PR	24-OCT-1997; 97US-0063120P.				
PR	PR	24-OCT-1997; 97US-0063121P.				
PR	PR	28-OCT-1997; 97US-0063540P.				
PR	PR	28-OCT-1997; 97US-0063541P.				
PR	PR	28-OCT-1997; 97US-0063544P.				
PR	PR	28-OCT-1997; 97US-0063564P.				
PR	PR	31-OCT-1997; 97US-0063734P.				
PR	PR	31-OCT-1997; 97US-0063870P.				
PR	PR	31-OCT-1997; 97US-0064103P.				
PR	PR	13-NOV-1997; 97US-0065311P.				
PR	PR	21-NOV-1997; 97US-0066120P.				
PR	PR	24-NOV-1997; 97US-0066466P.				
PR	PR	24-NOV-1997; 97US-0066772P.				
PR	PR	11-DEC-1997; 97US-0069335P.				
PR	PR	12-DEC-1997; 97US-0069425P.				
PR	PR	17-DEC-1997; 97US-0069870P.				

PR 22-JUN-1998; 98US-0090254P.
 PR 24-JUN-1998; 98US-0090429P.
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 PR 26-JUN-1998; 98US-0090862P.
 PR 26-JUN-1998; 98US-0090863P.
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 PR 01-JUL-1998; 98US-0091359P.
 PR 02-JUL-1998; 98US-0091544P.
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 PR 02-JUL-1998; 98US-0091486P.
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 PR 24-JUL-1998; 98US-0094006P.
 PR 04-AUG-1998; 98US-0095282P.
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PR 25-SEP-1998; 98US-0101786P.
 PR 29-SEP-1998; 98US-0102207P.
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 PR 29-SEP-1998; 98US-0102330P.
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 PR 30-SEP-1998; 98US-0102571P.
 PR 01-OCT-1998; 98US-0102684P.
 PR 01-OCT-1998; 98US-0102687P.
 Query Match 99.4%; Score 826.2; DB 7; Length 1016;
 Best Local Similarity 99.6%; Pred. No. 3.2e-241;
 Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 ATGAATGGCTTTGCGATCCTTTCGAGAAACCAATTTATCTCTCTGCTACTATTTCTT 60
 DB 22 ATGAATGGCTTTGCGATCCTTTCGAGAAACCAATTTATCTCTCTGCTACTATTTCTT 81
 QY 61 TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCGCTCTACCGCTGAAGTCTGTGCC 120
 DB 82 TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCGCTCTACCGCTGAAGTCTGTGCC 141
 QY 121 ACACACAAATTTACAGAGCCCAAGAGAGATGATGGTGAAGAAAGGAGATCCAGAGAA 180
 DB 142 ACACACAAATTTACAGAGCCCAAGAGAGATGATGGTGAAGAAAGGAGATCCAGAGAA 201
 QY 181 GAGGAAAGCATGCGAAAGTGGGACGATGGGGCCGAAAGGAATTAAGAGAACTGGGT 240
 DB 202 GAGGAAAGCATGCGAAAGTGGGACGATGGGGCCGAAAGGAATTAAGAGAACTGGGT 261
 QY 241 GATATGGGAGATCGGGCAATATTTGGCAAGACTGGGCCCATTTGGGAAGAGGAGTGAACAA 300
 DB 262 GATATGGGAGATCAGGCAATATTTGGCAAGACTGGGCCCATTTGGGAAGAGGAGTGAACAA 321
 QY 301 GGGGAAAAAGTTTGTCTGGAATACCTGGAGAAAAAGGCAAGCAGGACTCTCTGTGAT 360
 DB 322 GGGGAAAAAGTTTGTCTGGAATACCTGGAGAAAAAGGCAAGCAGGACTCTCTGTGAT 381
 QY 361 TGTGAAAGTACCGGAAATTTGTTGACAACTGGATATTAGTATTGCCGGCTCAAGACA 420
 DB 382 TGTGAAAGTACCGGAAATTTGTTGACAACTGGATATTAGTATTGCCGGCTCAAGACA 441
 QY 421 TCTATGAAGTTTGTCAAGATGTAGCAGGAGATTAGGGAACCTGAAGAGAAATTTCTAC 480
 DB 442 TCTATGAAGTTTGTCAAGATGTAGCAGGAGATTAGGGAACCTGAAGAGAAATTTCTAC 501
 QY 481 TACATCGTCAGGAAGAGAACTACAGGGAATCCCTAACCCACTGCGAGGATTCGGGT 540
 DB 502 TACATCGTCAGGAAGAGAACTACAGGGAATCCCTAACCCACTGCGAGGATTCGGGT 561
 QY 541 GGAATGCTAGCCATGCCCAGGATGAAGTCCCAACACACTCATCGCTGACTATTTGCC 600
 DB 562 GGAATGCTAGCCATGCCCAGGATGAAGTCCCAACACACTCATCGCTGACTATTTGCC 621
 QY 601 AAGAGTGGCTTTCTTGGGTGTTTCATTGGCGTGAATGACCTTTGAAAGGGAGGAGCAGTAC 660
 DB 622 AAGAGTGGCTTTCTTGGGTGTTTCATTGGCGTGAATGACCTTTGAAAGGGAGGAGCAGTAC 681
 QY 661 ATGTTACAGACAACTCCACTGCGAGAACTATAGCACTGAAGTGAAGGGGAAACCCAGC 720
 DB 682 ATGTTACAGACAACTCCACTGCGAGAACTATAGCACTGAAGTGAAGGGGAAACCCAGC 741
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XX
AC ACC86943;
XX
DT 05-AUG-2003 (first entry)
XX
DE Human secreted polypeptide PRO702-encoding cDNA, SEQ ID NO:99.
XX
XX Human; PRO; secreted protein; transmembrane protein;
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnary; gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
XX US2003036159-A1.
XX
PN
PD 20-FEB-2003.
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RESULT 12

ACA90292

ID ACA90292 standard; cdna; 1016 BP.

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KW	chondrocyte differentiation; tumour necrosis factor-alpha release; ss;

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XX AC ACC89399;
XX DT 11-AUG-2003 (first entry)
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XX KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
XX KW chondrocyte; proliferation; differentiation; cartilage disorder;
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; APPLICANT: Weber, Eric R.
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACIDS
; FILE REFERENCE: AU-5
; CURRENT APPLICATION NUMBER: US/09/535,521
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/125,913
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RESULT 5
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; APPLICANT: Weber, Eric R.
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; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
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;; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
;; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
;; FILE REFERENCE: AL-5
;; CURRENT APPLICATION NUMBER: US/09/535,521
;; CURRENT FILING DATE: 2000-03-24
;; EARLIER APPLICATION NUMBER: 60/125,913
;; EARLIER FILING DATE: 1999-03-24
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DB 36 GAAGTGTCTACTACTTCGGCGAGAGGCCCAAGAAATGGATCCAGGCCCGGTTTGCCTGCAG 95
QY 531 GATTCGGGGTGAATGCTAGCCATGCCAAGGATGAAGCTGCCAACAACACTCATCGCTGA 590
DB 96 CAAGCTCAAGGGCGGCTGGCCAGCATCCACAGCAAGAGAGAGAGGACTTCCTGGCCAG 155
QY 591 CTATGTTGCCAAGAGTGGCTTCCTTCGGGTGTTTCATTTGGCGTGAATGACCTTGAAGGGA 650
DB 156 GTATGCCAACAAGAGGCGACC-----TGGATTGGCCCTCCGGACCTTGGACAGAGA 206
QY 651 GGGACAGTACATGTTTCACAGACAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGG 710
DB 207 GGGGGAGTTTATCTGGATGGACGAGAACCCCT---GAACTATAGCAACTGGCGGCCCGG 263
QY 711 GGAACCCAGGACCCCTATGGTTCATGAGGACTGTGTGGAGATGCTGAGCTTGGCAGATG 770
DB 264 GGAGCCCAACAAGGGGGCCAGGGCGAGGAGTGGGTGATGTCAGGGGCTCGGGGCACTG 323
QY 771 GAATGACACAGAGTGC 786
DB 324 GAATGAGCCTTCTGC 339

RESULT 7
US-09-535-521-9/c
; Sequence 9, Application US/09535521
; Patent No. 6410714
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: AL-5
; CURRENT APPLICATION NUMBER: US/09/535,521
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/125,913
; EARLIER FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 384
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-535-521-9

Query Match 7.7%; Score 64; DB 4; Length 384;
Best Local Similarity 55.1%; Pred. No. 1.9e-10;
Matches 174; Conservative 0; Mismatches 130; Indels 12; Gaps 2;

QY 471 GAAATCTACTACATCGTCAGAGAGAGAACTACAGGGAAATCCCTAACCCACTGCAG 530
DB 349 GAAGTGTCTACTACTTCGGCGAGAGGCCCAAGAAATGGATCCAGGCCCGGTTTGCCTGCAG 290
QY 531 GATTCGGGGTGAATGCTAGCCATGCCAAGGATGAAGCTGCCAACAACACTCATCGCTGA 590
DB 289 CAAGCTCAAGGGCGGCTGGCCAGCATCCACAGCAAGAGAGAGAGGACTTCCTGGCCAG 230
QY 591 CTATGTTGCCAAGAGTGGCTTCCTTCGGGTGTTTCATTTGGCGTGAATGACCTTGAAGGGA 650
DB 229 GTATGCCAACAAGAGGCGACC-----TGGATTGGCCCTCCGGACCTTGGACAGAGA 179
QY 651 GGGACAGTACATGTTTCACAGACAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGG 710
DB 178 GGGGGAGTTTATCTGGATGGACGAGAACCCCT---GAACTATAGCAACTGGCGGCCCGG 122
QY 711 GGAACCCAGGACCCCTATGGTTCATGAGGACTGTGTGGAGATGCTGAGCTTGGCAGATG 770
DB 121 GGAGCCCAACAAGGGGGCCAGGGCGAGGAGTGGGTGATGTCAGGGGCTCGGGGCACTG 62
QY 771 GAATGACACAGAGTGC 786
DB 61 GAATGAGCCTTCTGC 46

RESULT 8
US-09-535-521-10
; Sequence 10, Application US/09535521
; Patent No. 6410714
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: AL-5
; CURRENT APPLICATION NUMBER: US/09/535,521
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/125,913
; EARLIER FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 10
; LENGTH: 417
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(417)
US-09-535-521-10

Query Match 7.7%; Score 64; DB 4; Length 417;
Best Local Similarity 55.1%; Pred. No. 2e-10;
Matches 174; Conservative 0; Mismatches 130; Indels 12; Gaps 2;

QY 471 GAAATCTACTACATCGTCAGAGAGAGAACTACAGGGAAATCCCTAACCCACTGCAG 530
DB 69 GAAGTGTCTACTACTTCGGCGAGAGGCCCAAGAAATGGATCCAGGCCCGGTTTGCCTGCAG 128
QY 531 GATTCGGGGTGAATGCTAGCCATGCCAAGGATGAAGCTGCCAACAACACTCATCGCTGA 590
DB 129 CAAGCTCAAGGGCGGCTGGCCAGCATCCACAGCAAGAGAGAGAGGACTTCCTGGCCAG 188
QY 591 CTATGTTGCCAAGAGTGGCTTCCTTCGGGTGTTTCATTTGGCGTGAATGACCTTGAAGGGA 650
DB 189 GTATGCCAACAAGAGGCGACC-----TGGATTGGCCCTCCGGACCTTGGACAGAGA 239
QY 651 GGGACAGTACATGTTTCACAGACAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGG 710
DB 240 GGGGGAGTTTATCTGGATGGACGAGAACCCCT---GAACTATAGCAACTGGCGGCCCGG 296
QY 711 GGAACCCAGGACCCCTATGGTTCATGAGGACTGTGTGGAGATGCTGAGCTTGGCAGATG 770
DB 297 GGAGCCCAACAAGGGGGCCAGGGCGAGGAGTGGGTGATGTCAGGGGCTCGGGGCACTG 356

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QY 771 GAATGACACAGAGTGC 786
Db 357 GAATGACGCTTCTGCG 372

RESULT 9
US-09-535-521-12/c
; Sequence 12, Application US/09535521
; Patent No. 6410714
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: AL-5
; CURRENT APPLICATION NUMBER: US/09/535,521
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/125,913
; EARLIER FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 417
; TYPE: DNA
; ORGANISM: Canis familiaris
; US-09-535-521-12

Query Match 7.7%; Score 64; DB 4; Length 417;
Best Local Similarity 55.1%; Pred. No. 2e-10;
Matches 174; Conservative 0; Mismatches 130; Indels 12; Gaps 2;

QY 471 GAAATCTTACTACATCGTCGAGGAGAGAGAACTACAGGGAATCCCTAACCCACTGCAG 530
Db 349 GAAGTGTCTACTTCTCGGAGAGAGCCCAAGAGTGGATCCAGGCCCGGTTTGCCTGCAG 290
QY 531 GATTGGGGTGAATGCTAGCCATGCCCAAGAGTGAAGCTGCCAACAACACTCATTCGCTGA 590
Db 289 CAAGCTGCAAGGGCGCTGCGCAGATCCACAGCAAGAGAGCAGACTTCTTGGCCAG 230
QY 591 CTATGTTGCCAAGAGTGGCTTCTTTCCGGGTGTTTCATTGGCGTGAATGACCTTGAAGGGA 650
Db 229 GTATGCCAACAGAGGGCACC-----TGGATTGGCTCCGGGACCTGGACAGAGA 179
QY 651 GGCACAGTACATGTTACAGACAACTCCACTGAGAGTGTGTGAGATGCTGAGCTCTGGCAGATG 710
Db 178 GGGGGAGTTTATCTGGATGGAGAGAACCCCT---GAACTATAGCAACTGGCGGCCCGG 122
QY 711 GGAACCCAGCGACCCCTATGGTCAAGAGTGTGTGAGATGCTGAGCTCTGGCAGATG 770
Db 121 GGAAGCCCAACAGGGGGCCAGGGCGAGGACTGCTGATGATGAGGGCTCGGGCAGTG 62
QY 771 GAATGACACAGAGTGC 786
Db 61 GAATGACGCTTCTGCG 46

RESULT 10
US-09-535-521-13
; Sequence 13, Application US/09535521
; Patent No. 6410714
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: AL-5
; CURRENT APPLICATION NUMBER: US/09/535,521
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/125,913
; EARLIER FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 13
; LENGTH: 423
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(423)
US-09-535-521-13

Query Match 7.7%; Score 64; DB 4; Length 423;
Best Local Similarity 55.1%; Pred. No. 2e-10;
Matches 174; Conservative 0; Mismatches 130; Indels 12; Gaps 2;

QY 471 GAAATCTTACTACATCGTCGAGGAGAGAGAACTACAGGGAATCCCTAACCCACTGCAG 530
Db 75 GAAGTGTCTACTTCTCGGAGAGAGCCCAAGAGTGGATCCAGGCCCGGTTTGCCTGCAG 134
QY 531 GATTGGGGTGAATGCTAGCCATGCCCAAGAGTGAAGCTGCCAACAACACTCATTCGCTGA 590
Db 135 CAAGCTGCAAGGGCGCTGCGCAGATCCACAGCAAGAGAGCAGACTTCTTGGCCAG 194
QY 591 CTATGTTGCCAAGAGTGGCTTCTTTCCGGGTGTTTCATTGGCGTGAATGACCTTGAAGGGA 650
Db 195 GTATGCCAACAGAGGGCACC-----TGGATTGGCTCCGGGACCTGGACAGAGA 245
QY 651 GGCACAGTACATGTTACAGACAACTCCACTGAGAGTGTGTGAGATGCTGAGCTCTGGCAGATG 710
Db 246 GGGGGAGTTTATCTGGATGGAGAGAACCCCT---GAACTATAGCAACTGGCGGCCCGG 302
QY 711 GGAACCCAGCGACCCCTATGGTCAAGAGTGTGTGAGATGCTGAGCTCTGGCAGATG 770
Db 303 GGAGGCCCAACAGGGGGCCAGGGCGAGGACTGCGTGATGATGAGGGGCTCGGGGCGAGTG 362
QY 771 GAATGACACAGAGTGC 786
Db 363 GAATGACGCTTCTGCG 378

RESULT 11
US-09-535-521-15/c
; Sequence 15, Application US/09535521
; Patent No. 6410714
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: AL-5
; CURRENT APPLICATION NUMBER: US/09/535,521
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/125,913
; EARLIER FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 423
; TYPE: DNA
; ORGANISM: Canis familiaris
; US-09-535-521-15

Query Match 7.7%; Score 64; DB 4; Length 423;
Best Local Similarity 55.1%; Pred. No. 2e-10;
Matches 174; Conservative 0; Mismatches 130; Indels 12; Gaps 2;

QY 471 GAAATCTTACTACATCGTCGAGGAGAGAGAACTACAGGGAATCCCTAACCCACTGCAG 530
Db 349 GAAGTGTCTACTTCTCGGAGAGAGCCCAAGAGTGGATCCAGGCCCGGTTTGCCTGCAG 290
QY 531 GATTGGGGTGAATGCTAGCCATGCCCAAGAGTGAAGCTGCCAACAACACTCATTCGCTGA 590
Db 289 CAAGCTGCAAGGGCGCTGCGCAGATCCACAGCAAGAGAGCAGACTTCTTGGCCAG 230
QY 591 CTATGTTGCCAAGAGTGGCTTCTTTCCGGGTGTTTCATTGGCGTGAATGACCTTGAAGGGA 650
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Db 229 GTATGCCAACAGAGGCGACC-----TGGATTGGCCCTCCGGGACCTGGACAGAGA 179
Qy 651 GGGACAGTACATGTTACAGACACACACTCCACTGCAGAACTATAGCAACTGGAATGAGGG 710
Db 178 GGGGGAGTTTATCTGATGCGAGAGAACCCCT---GAATATAGCAACTGGCGGCCGG 122
Qy 711 GGAACCCAGGACCCCTATGGTCATGAGCACTGTGTGAGATGCTGAGCTTGGCAGATG 770
Db 121 GGAGCCCAACACGGGGGCCAGGGCGAGGACTGCGTGATGATGCGAGGCTCGGGGCAGTG 62
Qy 771 GAATGACACAGAGTGC 786
Db 61 GAATGACGCTTCTGC 46

RESULT 12

US-09-535-521-16
; Sequence 16, Application US/09535521
; Patent No. 6410714
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
; FILE REFERENCE: AL-5
; CURRENT APPLICATION NUMBER: US/09/535,521
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/125,913
; EARLIER FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(561)
US-09-535-521-16

Query Match 7.7%; Score 64; DB 4; Length 561;
Best Local Similarity 55.1%; Pred. No. 2.4e-10;
Matches 174; Conservative 0; Mismatches 130; Indels 12; Gaps 2;
Qy 471 GAAATCTTACTACATCGTGCAGAGAGAGAACTACAGGAGATCCCTAACCCACTGCAG 530
Db 213 GAAATGCTACTACTTCGGCGAGAGGCCCAAGAGTGGATCCAGGCCCGGTTTGGCTGCAG 272
Qy 531 GATTCCGGGTGGAATCTAGCCATGCCCAAGGATGAAGTGCACACACTCATCGCTGA 590
Db 273 CAAGCTGCAGAGCGCGCTGCCAGCATCCACAGCCAGAGGAGAGGACTTCCTGGCCAG 332
Qy 591 CTATGTTGCCAAGAGTGGTCTTTTCGGGTGTTCTATTCGGCGTGAATGACCTTGAAGGGA 650
Db 333 GTATGCCAACAGAGAGGCCACC-----TGGATTGGCCCTCCGGGACCTGGACAGAGA 383
Qy 651 GGCACAGTACATGTTACAGACACACACTCCACTGCAGAACTATAGCAACTGGAATGAGGG 710
Db 384 GGGGAGTTTATCTGATGACAGAACCCCT---GAATATAGCAACTGGCGGCCGG 440
Qy 711 GGAACCCAGGACCCCTATGGTCATGAGCACTGTGTGAGATGCTGAGCTTGGCAGATG 770
Db 441 GGAGCCCAACACGGGGGCCAGGGCGAGGACTGCGTGATGATGACAGGCTCGGGGCAGTG 500
Qy 771 GAATGACACAGAGTGC 786
Db 501 GAATGACGCTTCTGC 516

RESULT 13

US-09-535-521-18/c
; Sequence 18, Application US/09535521

; Patent No. 6410714
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
; FILE REFERENCE: AL-5
; CURRENT APPLICATION NUMBER: US/09/535,521
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/125,913
; EARLIER FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-535-521-18

Query Match 7.7%; Score 64; DB 4; Length 561;
Best Local Similarity 55.1%; Pred. No. 2.4e-10;
Matches 174; Conservative 0; Mismatches 130; Indels 12; Gaps 2;
Qy 471 GAAATCTTACTACATCGTGCAGAGAGAGAACTACAGGAGATCCCTAACCCACTGCAG 530
Db 349 GAAATGCTACTACTTCGGCGAGAGGCCCAAGAGTGGATCCAGGCCCGGTTTGGCTGCAG 290
Qy 531 GATTCCGGGTGGAATCTAGCCATGCCCAAGGATGAAGTGCACACACTCATCGCTGA 590
Db 289 CAAGCTGCAGAGCGCGCTGGCCAGCATCCACAGCCAGAGGAGAGGACTTCCTGGCCAG 230
Qy 591 CTATGTTGCCAAGAGTGGTCTTTTCGGGTGTTCTATTCGGCGTGAATGACCTTGAAGGGA 650
Db 229 GTATGCCAACAGAGAGGCCACC-----TGGATTGGCCCTCCGGGACCTGGACAGAGA 179
Qy 651 GGCACAGTACATGTTACAGACACACACTCCACTGCAGAACTATAGCAACTGGAATGAGGG 710
Db 178 GGGGAGTTTATCTGATGACAGAACCCCT---GAATATAGCAACTGGCGGCCGG 122
Qy 711 GGAACCCAGGACCCCTATGGTCATGAGCACTGTGTGAGATGCTGAGCTTGGCAGATG 770
Db 121 GGAGCCCAACACGGGGGCCAGGGCGAGGACTGCGTGATGATGACAGGCTCGGGGCAGTG 62
Qy 771 GAATGACACAGAGTGC 786
Db 61 GAATGACGCTTCTGC 46

RESULT 14

US-09-535-521-19
; Sequence 19, Application US/09535521
; Patent No. 6410714
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
; FILE REFERENCE: AL-5
; CURRENT APPLICATION NUMBER: US/09/535,521
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/125,913
; EARLIER FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 624
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(624)
US-09-535-521-19

Query Match	7.7%;	Score 64;	DB 4;	Length 624;
Best Local Similarity	55.1%;	Pred. No. 2.6e-10;		
Matches 174;	Conservative 0;	Mismatches 130;	Indels 12;	Gaps 2;
Qy	471	GAATTTCTACTACATCTGTGCAGGAGAGAGAACTACAGGAATCCCTAACCCATCTGCAG	530	
Db	276	GAAAGTCTACTACTTTGGCGAGGAGCCCAAGATGGATCCAGGCCCGCTTTGCCCTGCAG	336	
Qy	531	GATTCGGGGTGGAAATGCTAGCCATGCCCAAGAGTGAAGCTGCCCAACACACTCATCGCTGA	590	
Db	336	CAAGCTGCAAGGGCGGCTGGCCAGCANTCCACAGCCAGAGAGCAGGACTTCTGTGCCAG	395	
Qy	591	CTATGTTGCCCAAGATGGCTTCTTCCTCGGGTGTCAATGGCGTGAATGAACCTTGAAGGGA	650	
Db	396	GTATGCCAACAGAGAGGGCACC-----TGGANTGGCCTCCGGGACCTGGACAGAGA	446	
Qy	651	GGGACAGTACATGTTTCACAGACACACTCCACTGCGAGACTATAGCAACTGGMATGAGGG	710	
Db	447	GGGGAGATTTATCTGGATGGACAGAGACCCCCCT---GAACTATAGCAACTGGCGGCCCGG	503	
Qy	711	GGAAACCCAGCCACCCCTTATGCTATGAGGACTCTGTGGAGATGCTTGAGCTCTGGCAGATG	770	
Db	504	GGAGCCCAACACGGGGGCCAGGCGAGGACTCGGTGATGATGCAGGGCTCGGGGCACTG	563	
Qy	771	GAATGACACAGAGTGC	786	
Db	564	GAATGACGCTTCTGC	579	

```

RESULT 15
US-09-535-521-21/c
; Sequence 21, Application US/09535521
; Patent No. 6410714
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: AL-5
; CURRENT APPLICATION NUMBER: US/09/535,521
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/125,913
; EARLIER FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 624
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-535-521-21

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Query Match	7.7%;	Score 64;	DB 4;	Length 624;
Best Local Similarity	55.1%;	Pred. No. 2.6e-10;		
Matches 174;	Conservative 0;	Mismatches 130;	Indels 12;	Gaps 2;
QY	471	GAATTTCTACTACATCGTCGAGGAGAGAGAACTACACGGGATCCCTAACCCACTCCAG	530	
Db	349	GAAGTGTCTACTTTCGGCGAGAGCCCGAGAAGTGGATCCAGGCCGGTTTGCTCGCAG	290	
QY	531	GATTCGGGGTGGAAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACACACACTCATCGTGTGA	590	
Db	289	CAAGCTGCAAGGGCGGCTGCCAGCATCCACAGCCAGAGGACGAGGACTTCTCTGGCCAG	230	
QY	591	CTATGTTGCCCAAGAGTGGCTTCTTCGGGTGTTCACTGGCGTGAATGACCTTGAAGAGGA	650	
Db	229	GTATGCCCAACAAGAGGGCAC-----TGGATTGGCTTCGGGGACCTGGGACAGAGA	179	
QY	651	GGGACAGTACATGTTACAGACAACACTCCACATGCAGAACTATAGCAACTCGAATGAGGG	710	
Db	178	GGGGAGTTTATCTGGATGAGCAGAGAACCCCT---GAACTATAGCAACTCGGGGCCCGG	122	
QY	711	GGAAACCCAGACCCCTTATGGTCA TGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATG	770	

1	PRIOR APPLICATION NUMBER: 60/081222	
2	PRIOR FILING DATE: 1998-04-09	
3	PRIOR APPLICATION NUMBER: 60/081955	
4	PRIOR FILING DATE: 1998-04-15	
5	PRIOR APPLICATION NUMBER: 60/081817	
6	PRIOR FILING DATE: 1998-04-15	
7	PRIOR APPLICATION NUMBER: 60/081819	
8	PRIOR FILING DATE: 1998-04-15	
9	PRIOR APPLICATION NUMBER: 60/081952	
10	PRIOR FILING DATE: 1998-04-15	
11	PRIOR APPLICATION NUMBER: 60/081938	
12	PRIOR FILING DATE: 1998-04-15	
13	PRIOR APPLICATION NUMBER: 60/082568	
14	PRIOR FILING DATE: 1998-04-21	
15	PRIOR APPLICATION NUMBER: 60/082569	
16	PRIOR FILING DATE: 1998-04-21	
17	PRIOR APPLICATION NUMBER: 60/082704	
18	PRIOR FILING DATE: 1998-04-22	
19	PRIOR APPLICATION NUMBER: 60/082804	
20	PRIOR FILING DATE: 1998-04-22	
21	PRIOR APPLICATION NUMBER: 60/082700	
22	PRIOR FILING DATE: 1998-04-22	
23	PRIOR APPLICATION NUMBER: 60/082797	
24	PRIOR FILING DATE: 1998-04-22	
25	PRIOR APPLICATION NUMBER: 60/082796	
26	PRIOR FILING DATE: 1998-04-23	
27	PRIOR APPLICATION NUMBER: 60/083336	
28	PRIOR FILING DATE: 1998-04-27	
29	PRIOR APPLICATION NUMBER: 60/083322	
30	PRIOR FILING DATE: 1998-04-28	
31	PRIOR APPLICATION NUMBER: 60/083392	
32	PRIOR FILING DATE: 1998-04-29	
33	PRIOR APPLICATION NUMBER: 60/083495	
34	PRIOR FILING DATE: 1998-04-29	
35	PRIOR APPLICATION NUMBER: 60/083496	
36	PRIOR FILING DATE: 1998-04-29	
37	PRIOR APPLICATION NUMBER: 60/083499	
38	PRIOR FILING DATE: 1998-04-29	
39	PRIOR APPLICATION NUMBER: 60/083545	
40	PRIOR FILING DATE: 1998-04-29	
41	PRIOR APPLICATION NUMBER: 60/083554	
42	PRIOR FILING DATE: 1998-04-29	
43	PRIOR APPLICATION NUMBER: 60/083558	
44	PRIOR FILING DATE: 1998-04-29	
45	PRIOR APPLICATION NUMBER: 60/083559	
46	PRIOR FILING DATE: 1998-04-29	
47	PRIOR APPLICATION NUMBER: 60/083500	
48	PRIOR FILING DATE: 1998-04-29	
49	PRIOR APPLICATION NUMBER: 60/083742	
50	PRIOR FILING DATE: 1998-04-30	
51	PRIOR APPLICATION NUMBER: 60/084366	
52	PRIOR FILING DATE: 1998-05-05	
53	PRIOR APPLICATION NUMBER: 60/084414	
54	PRIOR FILING DATE: 1998-05-06	
55	PRIOR APPLICATION NUMBER: 60/084441	
56	PRIOR FILING DATE: 1998-05-06	
57	PRIOR APPLICATION NUMBER: 60/084637	
58	PRIOR FILING DATE: 1998-05-07	
59	PRIOR APPLICATION NUMBER: 60/084639	
60	PRIOR FILING DATE: 1998-05-07	
61	PRIOR APPLICATION NUMBER: 60/084640	
62	PRIOR FILING DATE: 1998-05-07	
63	PRIOR APPLICATION NUMBER: 60/084598	
64	PRIOR FILING DATE: 1998-05-07	
65	PRIOR APPLICATION NUMBER: 60/084600	
66	PRIOR FILING DATE: 1998-05-07	
67	PRIOR APPLICATION NUMBER: 60/084627	
68	PRIOR FILING DATE: 1998-05-07	
69	PRIOR APPLICATION NUMBER: 60/084643	
70	PRIOR FILING DATE: 1998-05-07	
71	PRIOR APPLICATION NUMBER: 60/085339	
72	PRIOR FILING DATE: 1998-05-13	
73	PRIOR APPLICATION NUMBER: 60/085338	

1 PRIOR FILING DATE: 1998-05-13
2 PRIOR APPLICATION NUMBER: 60/085323
3 PRIOR FILING DATE: 1998-05-13
4 PRIOR APPLICATION NUMBER: 60/085582
5 PRIOR FILING DATE: 1998-05-15
6 PRIOR APPLICATION NUMBER: 60/085700
7 PRIOR FILING DATE: 1998-05-15
8 PRIOR APPLICATION NUMBER: 60/085689
9 PRIOR FILING DATE: 1998-05-15
10 PRIOR APPLICATION NUMBER: 60/085579
11 PRIOR FILING DATE: 1998-05-15
12 PRIOR APPLICATION NUMBER: 60/085580
13 PRIOR FILING DATE: 1998-05-15
14 PRIOR APPLICATION NUMBER: 60/085573
15 PRIOR FILING DATE: 1998-05-15
16 PRIOR APPLICATION NUMBER: 60/085704
17 PRIOR FILING DATE: 1998-05-15
18 PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.4%; Score 826.2; DB 9; Length 1016;
Best Local Similarity 99.6%; Pred. No. 5.7e-258;
Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 ATGATGGCTTGGCATCCTTCTCGAAGAAACCAATTTATCTCTCTGGTACTATTCTT 60
22 ATGATGGCTTGGCATCCTTCTCGAAGAAACCAATTTATCTCTCTGGTACTATTCTT 81
61 TTGCAAAATTCAGAGTCTGGGTCTGGATTTGATAGCCGCTCTACCGCTGAAGTCTGTGCC 120
82 TTGCAAAATTCAGAGTCTGGGTCTGGATTTGATAGCCGCTCTACCGCTGAAGTCTGTGCC 141
121 ACACACACAAATTCACAGGACCCCAAGAGATGATGGTGAAGAGAGATCCAGAGAA 180
142 ACACACAAATTCACAGGACCCCAAGAGATGATGGTGAAGAGAGATCCAGAGAA 201
181 GAGGAAAGATCGGCAAAAGTGGGAGCGATGGGGCGGAAAGAAATTAAGAGAACTGGGT 240
202 GAGGAAAGATCGGCAAAAGTGGGAGCGATGGGGCGGAAAGAAATTAAGAGAACTGGGT 261
241 GATATGGAGATCGGGGCAATATGGCAAGACTGGGCCATTTGGGAAGAGGGTGACAA 300
262 GATATGGAGATCGGGGCAATATGGCAAGACTGGGCCATTTGGGAAGAGGGTGACAA 321
301 GGGGAAAGATTTCTTGGAAATCTCGGAAAGCAAGCAAGTACTGTCTGTGAT 360
322 GGGGAAAGATTTCTTGGAAATCTCGGAAAGCAAGCAAGTACTGTCTGTGAT 381
361 TGTGAAGATACCGGAAATTTGTTGGCAACTGGATATTAGTATTCGCCGCTCAAGACA 420
382 TGTGAAGATACCGGAAATTTGTTGGCAACTGGATATTAGTATTCGCCGCTCAAGACA 441
421 TCTATGAAGTTTGTCAAGATGTGATAGCAGGATTTAGGAACTGAAGAGAAATTTCTAC 480
442 TCTATGAAGTTTGTCAAGATGTGATAGCAGGATTTAGGAACTGAAGAGAAATTTCTAC 501
481 TACATCGTGCAGGAGAGAGAACTTACAGGAAATCCCTAACCCACTCGAGATTCGGGGT 540
502 TACATCGTGCAGGAGAGAGAACTTACAGGAAATCCCTAACCCACTCGAGATTCGGGGT 561
541 GGAATGTAGCCATGCCCAAGATGAGCTGCCAACAATCTCATCTGCTGATGTGCC 600
562 GGAATGTAGCCATGCCCAAGATGAGCTGCCAACAATCTCATCTGCTGATGTGCC 621
601 AAGAGTGGCTTTCTTTCGGGTGTTTCATTTGGCGTGAATGACCTTGAAGAGGAGGACAGTAC 660
622 AAGAGTGGCTTTCTTTCGGGTGTTTCATTTGGCGTGAATGACCTTGAAGAGGAGGACAGTAC 681
661 ATGTTTCAGAGACACATCCCACTGAGAACTATAGCAACTGGAATGAGGGGAAACCCAGC 720
682 ATGTTTCAGAGACACATCCCACTGAGAACTATAGCAACTGGAATGAGGGGAAACCCAGC 741
721 GACCCCTATGTTGATGAGGACTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACA 780

Db 742 GACCCCTATGCTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACA 801
QY 781 GAGTGCCATCTTACCATGATCTTTGTTCTGTGAGTTCATCAAGAGAAAAAG 831
Db 802 GAGTGCCATCTTACCATGATCTTTGTTCTGTGAGTTCATCAAGAGAAAAAG 852

RESULT 2

US-09-978-697-96
Sequence 96, Application US/09978697
Patent No. US20020169284A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
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APPLICANT: Kljavin, Ivar J.
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APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C27
CURRENT APPLICATION NUMBER: US/09/978,697
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
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 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085704
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.4%; Score 826.2; DB 9; Length 1016;
 Best Local Similarity 99.6%; Pred. No. 5,7e-258;
 Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGAATGGCTTTGGCATCTCTGCTTCGAGAAACCAATTATCTCTGCTGCTACTATTCTTT 60
 DB 22 ATGAATGGCTTTGGCATCTCTGCTTCGAGAAACCAATTATCTCTGCTGCTACTATTCTTT 81
 QY 61 TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCGCTCTACCGCTGAAGTCTGTGCC 120

Db 82 TTCCAAATTCAGAGTCGGGTCTGGATATTGATAGCCGCTCTACCGCTGAAGTCTGTGCC 141
 QY 121 ACACACACAAATTCACAGAGCCCAAGAGAGATGATGTGAAAGAGAGATCCAGGAGAA 180
 Db 142 ACACACACAAATTCACAGAGCCCAAGAGAGATGATGTGAAAGAGAGATCCAGGAGAA 201
 QY 181 GAGGGAAGCATGCGAAATGCGAGAGCATGGGCGGAAAGAAATTAAGAGGAATCTGGT 240
 Db 202 GAGGGAAGCATGCGAAATGCGAGAGCATGGGCGGAAAGAAATTAAGAGGAATCTGGT 261
 QY 241 GATATGCGAGATCGGGGCCAATATGCGAAGACTGGGCCCATTTGGGAAGAGGGTGACAAA 300
 Db 262 GATATGCGAGATCGGGGCCAATATGCGAAGACTGGGCCCATTTGGGAAGAGGGTGACAAA 321
 QY 301 GGGGAAAAAGTTTGTGGAATACCTCGAGAAAAAGCAAGCAGTACTGTCTGTGAT 360
 Db 322 GGGGAAAAAGTTTGTGGAATACCTCGAGAAAAAGCAAGCAGTACTGTCTGTGAT 381
 QY 361 TGTGGAAGATACCGGAATTTGTTGGACAACTGGGATATTAGTATTGCTCCGCTCAAGACA 420
 Db 382 TGTGGAAGATACCGGAATTTGTTGGACAACTGGGATATTAGTATTGCTCCGCTCAAGACA 441
 QY 421 TGTGGAAGATTTGTTCAAGAAATGATAGCAGGATTTAGGGAATCTGAAGAGAAATTTCTAC 480
 Db 442 TGTGGAAGATTTGTTCAAGAAATGATAGCAGGATTTAGGGAATCTGAAGAGAAATTTCTAC 501
 QY 481 TACATGTCGAGAGAGAGAGAACTACAGGGAATCCCTAACCCACTCGCAGATTCGGGT 540
 Db 502 TACATGTCGAGAGAGAGAGAACTACAGGGAATCCCTAACCCACTCGCAGATTCGGGT 561
 QY 541 GGAATGCTAGCCATGCCCAAGATGAAGCTGCCAAGCACTCATCGCTGACTATGTGTGCC 600
 Db 562 GGAATGCTAGCCATGCCCAAGATGAAGCTGCCAAGCACTCATCGCTGACTATGTGTGCC 621
 QY 601 AGAGTGGCTTTCTGGGTGTTCAATGGCGTGAATGACCTTGAAGAGGAGGAGCAGTAC 660
 Db 622 AGAGTGGCTTTCTGGGTGTTCAATGGCGTGAATGACCTTGAAGAGGAGGAGCAGTAC 681
 QY 661 ATGTTCCACAGACAACTCCACTGAGAGAACTATAGCAACTGGAATGAGGGGAAACCCAGC 720
 Db 682 ATGTTCCACAGACAACTCCACTGAGAGAACTATAGCAACTGGAATGAGGGGAAACCCAGC 741
 QY 721 GACCCATGTCATGAGAGCTGTGTGAGATGCTGAGCTGTGCGATGTCGAGATGGAATGACACA 780
 Db 742 GACCCATGTCATGAGAGCTGTGTGAGATGCTGAGCTGTGCGATGTCGAGATGGAATGACACA 801
 QY 781 GAGTGCACTTTACCATGTACTTCTGTGAGTTCATCAAGAGAAAG 831
 Db 802 GAGTGCACTTTACCATGTACTTCTGTGAGTTCATCAAGAGAAAG 852

RESULT 3

US-09-978-192A-96
 ; Sequence 96, Application US/09978192A
 ; Patent No. US20020177553A1

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Geritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; TITLE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2630P1C9
 ; CURRENT APPLICATION NUMBER: US/09/978,192A
 ; CURRENT FILING DATE: 2001-10-15
 ; PRIOR APPLICATION NUMBER: 09/918585
 ; PRIOR FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/064249
 ; PRIOR FILING DATE: 1997-11-03
 ; PRIOR APPLICATION NUMBER: 60/065311
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;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.4%; Score 826.2; DB 9; Length 1016;

Best Local Similarity 99.6%; Pred. No. 5.7e-258; Indels 0; Gaps 0;
Matches 828; Conservative 0; Mismatches 3;

QY 1 ATGAATGGCTTTGTCATCCTTCTCGAAGAACCAATTTATCTCTCTGGTACTATTTCTT 60
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QY 61 TTGCAAAATTCAGAGTCGGGTCTGGATATTGATAGCGTCTTACCGCTGAAGTCTGTGCC 120
DB 82 TTGCAAAATTCAGAGTCGGGTCTGGATATTGATAGCGTCTTACCGCTGAAGTCTGTGCC 141
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DB 142 ACACACACAATTTTACACAGGACCCAAAGGAGATGATGTTGAAAAGGAGATCCAGGAGAA 201
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DB 322 GGGGAAAAGGTTTGTCTTGGAAATACCTTGGGAAAAGGCAAGCAGGTACTGTCTGTGAT 381
QY 361 TGTGGAAGATACCGGAAATTTGTTGGCAACTGGATATTAGTATTGCCCGCTCAAGACA 420
DB 382 TGTGGAAGATACCGGAAATTTGTTGGCAACTGGATATTAGTATTGCCCGCTCAAGACA 441
QY 421 TCTATGAAGTTTGTCAAGATGTGATAGCAGGGATTTAGGGAACCTGAAGAGAAATTTCTAC 480
DB 442 TCTATGAAGTTTGTCAAGATGTGATAGCAGGGATTTAGGGAACCTGAAGAGAAATTTCTAC 501
QY 481 TACATCGTGCAGGAAGAGAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGGGGT 540

Db 502 TACATGTCGAGAGAGAGAACTACAGGGATCCCTAACCCACTGCAGGANTCGGGGT 561
QY 541 GGAATGCTAGCCATGCCAAGATGAAGTGCACACACTCATGCTGATGTTGCC 600
Db 562 GGAATGCTAGCCATGCCAAGATGAAGTGCACACACTCATGCTGATGTTGCC 621
QY 601 AAGAGTGGCTTCTTTTCGGGTGTTTCATTGGCGTGAATGACCTTGAAGGGAGGGACAGTAC 660
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QY 661 ATGTTACAGACAACTCCACTGCAGACTATAGCAACTATAGCAACTGGAATGAGGGGAGCCAGC 720
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QY 781 GAGTGCATCTTACCATGTACTTCTGCTGTGAGTTTCATCAAGAGAAAAAG 831
Db 802 GAGTGCATCTTACCATGTACTTCTGCTGTGAGTTTCATCAAGAGAAAAAG 852

RESULT 4

US-09-999-832A-96
; Sequence 96, Application US/09999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
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; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC63
; CURRENT APPLICATION NUMBER: US/09/999,832A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
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;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.4%; Score 826.2; DB 9; Length 1016;
Best Local Similarity 99.6%; Pred. No. 5.7e-258;
Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 61 TTGCAATTCAGAGTCTGGGTCTGGATATTGATAGCGGTCTACCGTGAAGTCTGTGCC 120
DB 82 TTGCAATTCAGAGTCTGGGTCTGGATATTGATAGCGGTCTACCGTGAAGTCTGTGCC 141
QY 121 ACACACACAATTTCCACGAGGACCCAAAGGAGATGATGTTGAAAAAGGAGATCCAGAGAA 180
DB 142 ACACACACAATTTCCACGAGGACCCAAAGGAGATGATGTTGAAAAAGGAGATCCAGAGAA 201
QY 181 GAGGAAAGCATGGCAAGTGGGACCGCATGGGGCCGAAAGGAATTTAAAGAGAACTGGGT 240
DB 202 GAGGAAAGCATGGCAAGTGGGACCGCATGGGGCCGAAAGGAATTTAAAGAGAACTGGGT 261
QY 241 CATATGGGAGATCGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGAGGAGGTGACAA 300
DB 262 CATATGGGAGATCGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGAGGAGGTGACAA 321
QY 301 GGGGAAAAAGGTTTGTGGGAATACCTGGGAGAAAAAGGCAAAAGAGGTACTGTCTGTAT 360
DB 322 GGGGAAAAAGGTTTGTGGGAATACCTGGGAGAAAAAGGCAAAAGAGGTACTGTCTGTAT 381
QY 361 TGTGGAAGATACCGGAAATTTTGTGGCAACTGTGATATTAGTATTGCCGGCTCAAGACA 420
DB 382 TGTGGAAGATACCGGAAATTTTGTGGCAACTGTGATATTAGTATTGCCGGCTCAAGACA 441
QY 421 TCTATGAAGTTTGTCAAGAAATGTGATAGCGGATAGGGAATCTGAAAGAAATTTCTAC 480
DB 442 TCTATGAAGTTTGTCAAGAAATGTGATAGCGGATAGGGAATCTGAAAGAAATTTCTAC 501
QY 481 TACATCGTCAGGAGAGAGAACTACAGGGAATCCCTACCCACTGCAGATTCGGGT 540
DB 502 TACATCGTCAGGAGAGAGAACTACAGGGAATCCCTACCCACTGCAGATTCGGGT 561
QY 541 GGAATGCTAGCCATGCCCAAGGATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 600
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QY 601 AAGAGTGGCTTTCTTCGGGTGTTTCAATTGGGTGATGACCTTGAAGGGGAGGACAGTAC 660
DB 622 AAGAGTGGCTTTCTTCGGGTGTTTCAATTGGGTGATGACCTTGAAGGGGAGGACAGTAC 681
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DB 742 GACCCCTATGTCATGAGGACTGTGTGAGATGCTGAGCTCTGCAGATGGAATGACACA 801
QY 781 GAGTGGCAATCTTACCATGTACTTTGTCTGTGAGTTTCAAGAGAAAAAG 831
DB 802 GAGTGGCAATCTTACCATGTACTTTGTCTGTGAGTTTCAAGAGAAAAAG 852

RESULT 5
US-09-978-189-96
; Sequence 96, Application US/09978189
; Publication No. US2003004102A1

; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
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 ; APPLICANT: Shelton, David L.
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 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2630PIC7
 ; CURRENT APPLICATION NUMBER: US/09/978,189
 ; PRIOR FILING DATE: 2001-10-15
 ; PRIOR APPLICATION NUMBER: 09/918585
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Query Match 99.4%; Score 826.2; DB 10; Length 1016;
Best Local Similarity 99.6%; Pred. No. 5.7e-258;
Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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22 ATGAATGGCTTTGATCTCTTTCGAAGAAACCAATTTATCTCTCTGTAATTTCTT 81
61 TTGCAAAATTCAGAGTCGTGGGTCTGGATATTTGATAGCCGTCCTACCGCTGAAGTCGTGCC 120
82 TTGCAAAATTCAGAGTCGTGGGTCTGGATATTTGATAGCCGTCCTACCGCTGAAGTCGTGCC 141
121 ACACACAAATTTCCACGAGCCCAAGAGGATGATGGTGAAGAGGAGATCCAGAGAA 180
142 ACACACAAATTTCCACGAGCCCAAGAGGATGATGGTGAAGAGGAGATCCAGAGAA 201
181 GAGGAAAGCATGCGCAAGTGGGACGATGGGCCCGAAAGGAATTAAGGAGAACTGGGT 240
202 GAGGAAAGCATGCGCAAGTGGGACGATGGGCCCGAAAGGAATTAAGGAGAACTGGGT 261

241 GATATGGAGATCGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAAGAGGTGACAAA 300
262 GATATGGGAGATCAGGCAATATTGGCAAGACTGGGCCCATTTGGGAAAGAGGTGACAAA 321
301 GGGGAAAAGGTTTGGTGGAAATACCTGGGAGAAAAGGCAAGGAGTACTGTCTGTGAT 360
322 GGGGAAAAGGTTTGGTGGAAATACCTGGGAGAAAAGGCAAGGAGTACTGTCTGTGAT 381
361 TGTGAAAGATACCGGAAATTTGTTGGCAACTGATGATATTAGTATTGCCCGCTCAAGACA 420
382 TGTGAAAGATACCGGAAATTTGTTGGCAACTGATGATATTAGTATTGCCCGCTCAAGACA 441
421 TCTATGAAGTTTGTCAAGAAATGTATAGCAGGATATTAGGAAACTGAAGAAATTTCTAC 480
442 TCTATGAAGTTTGTCAAGAAATGTATAGCAGGATATTAGGAAACTGAAGAAATTTCTAC 501
481 TACATCGTGCAGGAGAGAAAGAACTACAGGGAATCCCTAACCCCACTGCAGGATTCGGGGT 540
502 TACATCGTGCAGGAGAGAAAGAACTACAGGGAATCCCTAACCCCACTGCAGGATTCGGGGT 561
541 GGAATGTAGCATGCCCAAGGATGAAGTCCCAACACACTCATCGCTGACTATGTGGC 600
562 GGAATGTAGCATGCCCAAGGATGAAGTCCCAACACACTCATCGCTGACTATGTGGC 621
601 AAGAGTGGCTTTCTTTGGGTTGTTCAATGGGCTGATGACCTTGAAGGGAGGACAGTAC 660
622 AAGAGTGGCTTTCTTTGGGTTGTTCAATGGGCTGATGACCTTGAAGGGAGGACAGTAC 681
661 ATGTTTCAACAGACACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGAAACCCAGC 720
682 ATGTTTCAACAGACACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGAAACCCAGC 741
721 GACCCCTATGGTCATGAGGATGTTGGAGATGCTGAGCTCTGCGAGATGCAATGACACA 780
742 GACCCCTATGGTCATGAGGATGTTGGAGATGCTGAGCTCTGCGAGATGCAATGACACA 801
781 GAGTGCATCTTACCATGATCTTTGCTGTGAGTTCATCAAGAGAAAAAG 831
802 GAGTGCATCTTACCATGATCTTTGCTGTGAGTTCATCAAGAGAAAAAG 852

RESULT 6
US-09-978-608A-96
; Sequence 96, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.


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; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 96
; LENGTH: 1016
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-978-608A-96

Query Match      99.4%; Score 826.2; DB 10; Length 1016;
Best Local Similarity 99.6%; Pred. No. 5.7e-258;
Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGAATGGCTTTCATCCTCTCGAGAAACCAATTTATCTCTCTGTACTATTCTTT 60
Db 22 ATGAATGGCTTTCATCCTCTCGAGAAACCAATTTATCTCTCTGTACTATTCTTT 81
QY 61 TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGCTCTACCGTGAAGTCTGTGCC 120
Db 82 TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGCTCTACCGTGAAGTCTGTGCC 141
QY 121 ACACACACAATTTCCAGAGCCCAAGAGATGATGTGTGAAAAGAGATCCAGAGGAA 180
Db 142 ACACACACAATTTCCAGAGCCCAAGAGATGATGTGTGAAAAGAGATCCAGAGGAA 201
QY 181 GAGGAAAGCATGGCAAAAGTGGACGCGATGGGCCGCGAAGAAATTAAGGAGAACTCGGT 240
Db 202 GAGGAAAGCATGGCAAAAGTGGACGCGATGGGCCGCGAAGAAATTAAGGAGAACTCGGT 261
QY 241 GATATGGGAGATCGGGGCAATATTGGCAAGACTGGGCCATTTGGGAAGAGGGTGACAAA 300
Db 262 GATATGGGAGATCGGGGCAATATTGGCAAGACTGGGCCATTTGGGAAGAGGGTGACAAA 321
QY 301 GGGGAAAAAGGTTTGTCTTGGATACCTCGAGAAAAAGGCAAGAGGAGTCTGTCTGTAT 360
Db 322 GGGGAAAAAGGTTTGTCTTGGATACCTCGAGAAAAAGGCAAGAGGAGTCTGTCTGTAT 381
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RESULT 7
US-09-978-585A-96
; Sequence 96, Application US/09978585A
; Publication NO. US20030049633A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Kapier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C15
; CURRENT APPLICATION NUMBER: US/09/978,585A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 96
; LENGTH: 1016
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-978-585A-96

Query Match      99.4%; Score 826.2; DB 10; Length 1016;
Best Local Similarity 99.6%; Pred. No. 5.7e-258;
Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGAATGGCTTTCATCCTCTCGAGAAACCAATTTATCTCTCTGTACTATTCTTT 60
Db 22 ATGAATGGCTTTCATCCTCTCGAGAAACCAATTTATCTCTCTGTACTATTCTTT 81
QY 61 TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGCTCTACCGTGAAGTCTGTGCC 120
Db 82 TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGCTCTACCGTGAAGTCTGTGCC 141
QY 121 ACACACACAATTTCCAGAGCCCAAGAGATGATGTGTGAAAAGAGATCCAGAGGAA 180
Db 142 ACACACACAATTTCCAGAGCCCAAGAGATGATGTGTGAAAAGAGATCCAGAGGAA 201
QY 181 GAGGAAAGCATGGCAAAAGTGGACGCGATGGGCCGCGAAGAAATTAAGGAGAACTCGGT 240
Db 202 GAGGAAAGCATGGCAAAAGTGGACGCGATGGGCCGCGAAGAAATTAAGGAGAACTCGGT 261
QY 241 GATATGGGAGATCGGGGCAATATTGGCAAGACTGGGCCATTTGGGAAGAGGGTGACAAA 300
Db 262 GATATGGGAGATCGGGGCAATATTGGCAAGACTGGGCCATTTGGGAAGAGGGTGACAAA 321
QY 301 GGGGAAAAAGGTTTGTCTTGGATACCTCGAGAAAAAGGCAAGAGGAGTCTGTCTGTAT 360
Db 322 GGGGAAAAAGGTTTGTCTTGGATACCTCGAGAAAAAGGCAAGAGGAGTCTGTCTGTAT 381
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QY 361 TGTGGAAGATACCGGAATTTGTTGGCAACTGGATATTAGTATTCCCGGCTCAAGACA 420
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 Db 502 TACATCTGCGAGGAAGAACTACAGGGAATCCCTAACCCACTGCGAGGATTCGGGGT 561
 QY 541 GGAATGTACCATGCCAGGATGAAGCTGCGACACACTCATGCTGACTATTTGCC 600
 Db 562 GGAATGTACCATGCCAGGATGAAGCTGCGACACACTCATGCTGACTATTTGCC 621
 QY 601 AAGAGTGGCTTCNTTCGGGTGTTTCATGGCGTGAATGACCTTGAAGGGGAGGGAAGTAC 660
 Db 622 AAGAGTGGCTTCNTTCGGGTGTTTCATGGCGTGAATGACCTTGAAGGGGAGGGAAGTAC 681
 QY 661 ATGTTACACACACACTCCTGCGAGAACTATAGCAACTGGAATGAGGGGACCCGAC 720
 Db 682 ATGTTACACACACACTCCTGCGAGAACTATAGCAACTGGAATGAGGGGACCCGAC 741
 QY 721 GACCCCTATGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACA 780
 Db 742 GACCCCTATGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACA 801
 QY 781 GAGTGCATCTTACCATGACTTGTCTGTGAGTTTCATCAGAGAAAAAG 831
 Db 802 GAGTGCATCTTACCATGACTTGTCTGTGAGTTTCATCAGAGAAAAAG 852

RESULT 8

US-09-978-191A-96
 ; Sequence 96, Application US/09978191A
 ; Publication No. US20030050239A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Deanoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gottard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James;
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; TITLE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2630F1C4
 ; CURRENT APPLICATION NUMBER: US/09/978,191A
 ; CURRENT FILING DATE: 2001-10-15
 ; PRIOR APPLICATION NUMBER: 09/918585
 ; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
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;; PRIOR APPLICATION NUMBER: 60/085573
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.4%; Score 826.2; DB 10; Length 1016;
Best Local Similarity 99.6%; Pred. No. 5.7e-258;
Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGAATGGCTTTTCATCCTTCTTGAAGAAACCAATTTATCTCTCTGGTACTATTCTT 60
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QY 22 ATGAATGGCTTTTCATCCTTCTTGAAGAAACCAATTTATCTCTCTGGTACTATTCTT 81
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QY 61 TTGCAATTCAGAGTCTGGGTCTGGATATTGATAGCGTCTCTACCGCTGAAGTCTGTGCC 120
DB |||||
QY 82 TTGCAATTCAGAGTCTGGGTCTGGATATTGATAGCGTCTCTACCGCTGAAGTCTGTGCC 141
DB |||||
QY 121 ACACACACAAATTTCCACAGGACCCAAAGGAGATGATGTTGAAAAAGAGATCCAGAGAA 180
DB |||||
QY 142 ACACACACAAATTTCCACAGGACCCAAAGGAGATGATGTTGAAAAAGAGATCCAGAGAA 201
DB |||||
QY 181 GAGGAAAGCATGCGAAAGTGGGACGATCGGGCCGAAAGAAATTAAGAGAACTGGGT 240
DB |||||
QY 202 GAGGAAAGCATGCGAAAGTGGGACGATCGGGCCGAAAGAAATTAAGAGAACTGGGT 261
DB |||||
QY 241 GATATGGGAGATCGGGCAATATTGGCAACACTGGGCCATTCGGGAAGAGGTGACAA 300
DB |||||
QY 262 GATATGGGAGATCAGGCAATATTGGCAACACTGGGCCATTCGGGAAGAGGTGACAA 321
DB |||||
QY 301 GGGGAAAAAGGTTTGTGGAATACCTGGGAAAAAGGCAAGCAAGTACTGTCTGTGAT 360
DB |||||
QY 322 GGGGAAAAAGGTTTGTGGAATACCTGGGAAAAAGGCAAGCAAGTACTGTCTGTGAT 381
DB |||||
QY 361 TGTGAGAGTACCGGAAATTTGTTGGCACTGGATATTAGTATTCGCCGCTCAGACA 420
DB |||||
QY 382 TGTGAGAGTACCGGAAATTTGTTGGCACTGGATATTAGTATTCGCCGCTCAGACA 441
DB |||||
QY 421 TCTATGAAGTTTGTCAAGAATGTGATAGCAGGATTAGGAAACTGAAGAGAAATTTCTAC 480
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QY 442 TCTATGAAGTTTGTCAAGAATGTGATAGCAGGATTAGGAAACTGAAGAGAAATTTCTAC 501
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QY 481 TACATCTGCAGGAGAGAACTACAGGATTCCTAACCCACTGCAGGATTCGGGT 540
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QY 502 TACATCTGCAGGAGAGAACTACAGGATTCCTAACCCACTGCAGGATTCGGGT 561
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QY 541 GGAATGCTAGCCATGCCCCAAGGATGAAGCTGCCAAACACACTCATCTGACTATGTTGCC 600
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QY 562 GGAATGCTAGCCATGCCCCAAGGATGAAGCTGCCAAACACACTCATCTGACTATGTTGCC 621
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QY 601 AAGAGTGGCTTCTTTCGGGTGTTTCATTGGCGTGAATGACCTTGAAGGAGGACAGTAC 660
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QY 622 AAGAGTGGCTTCTTTCGGGTGTTTCATTGGCGTGAATGACCTTGAAGGAGGACAGTAC 681
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QY 742 GACCCCTATGCTATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACAA 801
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QY 781 GAGTCCATCTTACCATGTACTTCTGTGTGAGTTTCATCAAGAGAAAAAG 831
 Db 802 GAGTCCATCTTACCATGTACTTCTGTGTGAGTTTCATCAAGAGAAAAAG 852

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 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
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 ; APPLICANT: Kijavlin, Ivar J.
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 ; APPLICANT: Napier, Mary A.
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 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; TITLE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2630P1C17
 ; CURRENT APPLICATION NUMBER: US/09/978,403A
 ; CURRENT FILING DATE: 2002-03-19
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 ; PRIOR APPLICATION NUMBER: 60/083322

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; PRIOR FILING DATE: 1998-05-15

Query Match          99.4%; Score 826.2; DB 10; Length 1016;
Best Local Similarity 99.6%; Pred. No. 5.7e-258;
Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGAATGGCTTTCATCTGCTTTCGAAAGAAACCAATTTATCTCTCTGGTACTATTTCTT 60
Db 22 ATGAATGGCTTTCATCTGCTTTCGAAAGAAACCAATTTATCTCTCTGGTACTATTTCTT 81
QY 61 TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGCTAGAGTCTGTGCC 120

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Db 82 TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGCTCTACCGCTGAAGTCTGTGCC 141
QY 121 ACACACACAAATTTTCCACAGGAGCCCAAGAGGAGATGATGTGTAAGAGGAGATCCAGGAGAA 180
Db 142 ACACACACAAATTTTCCACAGGAGCCCAAGAGGAGATGATGTGTAAGAGGAGATCCAGGAGAA 201
QY 181 GAGGGAAGCATGGCAAAAGTGGACCGATGGGGCCGAAAGGAATTAAGAGGAATCTGGGT 240
Db 202 GAGGGAAGCATGGCAAAAGTGGACCGATGGGGCCGAAAGGAATTAAGAGGAATCTGGGT 261
QY 241 GATATGGGAGATCGGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAAGAGGGTGACAAA 300
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QY 301 GGGGAAAAAGGTTTGTCTTGGATACCTGGGAAAAAGGCAAGCAGGTACTGTCTGTGAT 360
Db 322 GGGGAAAAAGGTTTGTCTTGGATACCTGGGAAAAAGGCAAGCAGGTACTGTCTGTGAT 381
QY 361 TGTGGAAGATACCGGAAATTTGTTGGCAACTGATATTAGTATTGCCCCGCTCAAGACA 420
Db 382 TGTGGAAGATACCGGAAATTTGTTGGCAACTGATATTAGTATTGCTCGGCTCAAGACA 441
QY 421 TCTATGAAGTTTGTCAAGATGTGATAGAGGATTTAGGGAAAACTGAAGAGAAATTTCTAC 480
Db 442 TCTATGAAGTTTGTCAAGATGTGATAGAGGATTTAGGGAAAACTGAAGAGAAATTTCTAC 501
QY 481 TACATCGTGCAGGAGAGAGAACTACAGGGAATCCCTTAACCCACTGCAGGATTCGGGGT 540
Db 502 TACATCGTGCAGGAGAGAGAACTACAGGGAATCCCTTAACCCACTGCAGGATTCGGGGT 561
QY 541 GGAATGTAGCCATGCCCAAGGATGAAGCTGCCAACACACTCATCTGCTGACTATGTTGCC 600
Db 562 GGAATGTAGCCATGCCCAAGGATGAAGCTGCCAACACACTCATCTGCTGACTATGTTGCC 621
QY 601 AAGAGTGGCTTCTTTTCGGGTGTTTTCATTTGGGTGATGACCTTGAAGGGAGGACAGTAC 660
Db 622 AAGAGTGGCTTCTTTTCGGGTGTTTTCATTTGGGTGATGACCTTGAAGGGAGGACAGTAC 681
QY 661 ATGTTTCACAGACAACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGGAACCCAGC 720
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QY 721 GACCCCTATGTCATGAGGACTGTGGAGATGTCGAGCTGTCGAGATGGAATGACACA 780
Db 742 GACCCCTATGTCATGAGGACTGTGGAGATGTCGAGCTGTCGAGATGGAATGACACA 801
QY 781 GAGTGGCAATCTTACCATGTAATTTGTTGCTGTGAGTTTCAAGAGAAAAAG 831
Db 802 GAGTGGCAATCTTACCATGTAATTTGTTGCTGTGAGTTTCAAGAGAAAAAG 852

RESULT 10
US-09-978-564A-96
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; Publication No. US20030050241A1
; GENERAL INFORMATION:
; APPLICANT: Ashtenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavini, Ivar J.

```

APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Thomas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Acids and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C25
CURRENT APPLICATION NUMBER: US/09/978,564A
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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Query Match 99.4%; Score 826.2; DB 10; Length 1016;

Best Local Similarity 99.6%; Field No. 5.7e-258;
 Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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 22 ATGAATGGCTTTGTCATCCCTTTCGAGAAACCAATTTATCTCCTGCTACTATTCTT 81
 61 TTGCAATTCAGAGTCTGGTCTGATATTGATAGCCCTCTACCGCTGAAGTCTGTGCC 120
 82 TTGCAATTCAGAGTCTGGTCTGATATTGATAGCCCTCTACCGCTGAAGTCTGTGCC 141
 121 ACACACACAAATTCACAGGACCCAAAGAGAGATGATGTTGAAAGAGATCCAGAGAA 180
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 181 GAGGAAAGATCGGCAAGTGGAGCGCATGGGGCCGAAAGGAATTAAGAGAACTGGGT 240
 202 GAGGAAAGATCGGCAAGTGGAGCGCATGGGGCCGAAAGGAATTAAGAGAACTGGGT 261
 241 GATATGGGAGATCGGGCAATATTCGAGAGCTGGCCCATTTGGGAGAGAGGTGACAAA 300
 262 GATATGGGAGATCGGGCAATATTCGAGAGCTGGCCCATTTGGGAGAGAGGTGACAAA 321
 301 GGGGAAAAAGTTTGTCTGGAAATACCTGGAGAAAGCAAGCAGGTACTGTCTGTGAT 360
 322 GGGGAAAAAGTTTGTCTGGAAATACCTGGAGAAAGCAAGCAGGTACTGTCTGTGAT 381
 361 TGTGGAGATACCGGAATTTGTTGGCAATCTGGATATTAGTATTCCTGGCTCAAGACA 420
 382 TGTGGAGATACCGGAATTTGTTGGCAATCTGGATATTAGTATTCCTGGCTCAAGACA 441
 421 TCTATGAAGTTTCTCAAGAAATCTAGCAGGATTTAGGAAATCTGAAGAGAAATTTCTAC 480
 442 TCTATGAAGTTTCTCAAGAAATCTAGCAGGATTTAGGAAATCTGAAGAGAAATTTCTAC 501
 481 TACATCGTCAGAGAGAGAGAACTACAGGAAATCCCTTAACCCCTGAGGATTCGGGGT 540

Db 502 TACATCGTGCAGGAAGAGAACTACAGGAATCCCTTAACCCACTGCAGGATTCGGGGT 561
 QY 541 GGAATGCTAGCCATGCCCAAGGATGAAGCTGCACACACACTCATCGCTGACTATGTTGCC 600
 Db 562 GGAATGCTAGCCATGCCCAAGGATGAAGCTGCACACACACTCATCGCTGACTATGTTGCC 621
 QY 601 AAGAGTGGCTTTCTTTCGGGTGTTTATTTGGCGTGAATGACCTTGAAGAGGGGACAGTAC 660
 Db 622 AAGAGTGGCTTTCTTTCGGGTGTTTATTTGGCGTGAATGACCTTGAAGAGGGGACAGTAC 681
 QY 661 ATGTTTCACAGACACACTCCCACTGCAGAACTATAGCAACTGGAATGAGGGGGAACCCAGC 720
 Db 682 ATGTTTCACAGACACACTCCCACTGCAGAACTATAGCAACTGGAATGAGGGGGAACCCAGC 741
 QY 721 GACCCCTATGCTCATGAGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACA 780
 Db 742 GACCCCTATGCTCATGAGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACA 801
 QY 781 GAGTGCCTATTTACCATCTACTTTTGTCTGTGAGTTTCATCAGAGAGAAAAAG 831
 Db 802 GAGTGCCTATTTACCATCTACTTTTGTCTGTGAGTTTCATCAGAGAGAAAAAG 852

RESULT 11
 US-09-999-833A-96
 ; Sequence 96, Application US/09999833A
 ; Publication No. US20030054405A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2630F1C65
 ; CURRENT APPLICATION NUMBER: US/09/999,833A
 ; PRIOR FILING DATE: 2001-10-24
 ; PRIOR APPLICATION NUMBER: 09/918585
 ; PRIOR FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/064249
 ; PRIOR FILING DATE: 1997-11-03
 ; PRIOR APPLICATION NUMBER: 60/065311
 ; PRIOR FILING DATE: 1997-11-13
 ; PRIOR APPLICATION NUMBER: 60/066364
 ; PRIOR FILING DATE: 1997-11-21
 ; PRIOR APPLICATION NUMBER: 60/077450
 ; PRIOR FILING DATE: 1998-03-10
 ; PRIOR APPLICATION NUMBER: 60/077632

PRIOR APPLICATION NUMBER: 60/082565	PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082569	PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082704	PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082804	PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082700	PRIOR FILING DATE: 1998-04-22
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PRIOR APPLICATION NUMBER: 60/082796	PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336	PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322	PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083495	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083496	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083499	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083499	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083545	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083554	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083558	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083559	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083500	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083742	PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366	PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414	PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084441	PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084637	PRIOR FILING DATE: 1998-05-07
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PRIOR APPLICATION NUMBER: 60/084640	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084598	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084598	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084600	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084627	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084643	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085339	PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085338	PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085323	PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085582	PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700	PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085689	PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579	PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580	PRIOR FILING DATE: 1998-05-15

; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085573
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085704
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.4%; Score 826.2; DB 10; Length 1016;
 Best Local Similarity 99.6%; Pred. No. 5.7e-258;
 Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	1	ATGAATGGCTTTGATCCCTTCTGCTTCGAAGAACCAATTTATCTCTCTCTGCTACTATTTCTT	60
Db	22	ATGAATGGCTTTGATCCCTTCTGCTTCGAAGAACCAATTTATCTCTCTCTGCTACTATTTCTT	81
Qy	61	TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATGCGCTCTACCGCTCAAGTCTGTGCC	120
Db	82	TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATGCGCTCTACCGCTCAAGTCTGTGCC	141
Qy	121	ACACACAAATTTACACAGGACCCAAAGAGATGATGTTGAAAGAGGAGATCCAGGAA	180
Db	142	ACACACAAATTTACACAGGACCCAAAGAGATGATGTTGAAAGAGGAGATCCAGGAA	201
Qy	181	GAGGAAAGCATGCGAAAGTGGGACCGTGGGCGGAAGGAATTAAGGAGACTGGT	240
Db	202	GAGGAAAGCATGCGAAAGTGGGACCGTGGGCGGAAGGAATTAAGGAGACTGGT	261
Qy	241	GATATGGAGATCGGGCAATATTGCAAGACTGGGCCCATTTGGGAAGAGGGTGACAAA	300
Db	262	GATATGGAGATCGGGCAATATTGCAAGACTGGGCCCATTTGGGAAGAGGGTGACAAA	321
Qy	301	GGGGAAGAGTTTGTCTGGAATACCTGAGAAAGCGCAAGCAAGTACTGTCTGTGAT	360
Db	322	GGGGAAGAGTTTGTCTGGAATACCTGAGAAAGCGCAAGCAAGTACTGTCTGTGAT	381
Qy	361	TGTGGAAGATPACCGAAATTTGTGACAACTGGATATTAGTATTGCCCCGGCTCAAGACA	420
Db	382	TGTGGAAGATPACCGAAATTTGTGACAACTGGATATTAGTATTGCCCCGGCTCAAGACA	441
Qy	421	TCATGAGTTTGTCAAGATGTGATGATGATGATGATGATGATGATGATGATGATGATGAT	480
Db	442	TCATGAGTTTGTCAAGATGTGATGATGATGATGATGATGATGATGATGATGATGATGAT	501
Qy	481	TACATCGTGCAGAGAGAGAACTACAGGAAATCCCTAACCCACTGCAGGATTCGGGT	540
Db	502	TACATCGTGCAGAGAGAGAACTACAGGAAATCCCTAACCCACTGCAGGATTCGGGT	561
Qy	541	GGAATGCTAGCTAGCCATGCCAAGAGATGAGCTGCCAACACATCATCGTACTATTTGCC	600
Db	562	GGAATGCTAGCTAGCCATGCCAAGAGATGAGCTGCCAACACATCATCGTACTATTTGCC	621
Qy	601	AAGAGTGGCTTTCTCGGTGTTTCATTGGCGTGAATGACCTTGAAGGGGAGGACAGTAC	660
Db	622	AAGAGTGGCTTTCTCGGTGTTTCATTGGCGTGAATGACCTTGAAGGGGAGGACAGTAC	681
Qy	661	ATGTTCAACAGACAACTCCATCGCAGAACTATGCAAACTGGAATGAGGGGGAACCCAGC	720
Db	682	ATGTTCAACAGACAACTCCATCGCAGAACTATGCAAACTGGAATGAGGGGGAACCCAGC	741
Qy	721	GACCCCTATGTTATGAGCACTGTGTGAGATGCTGAGCTCTGCAAGATGAATGACACA	780
Db	742	GACCCCTATGTTATGAGCACTGTGTGAGATGCTGAGCTCTGCAAGATGAATGACACA	801
Qy	781	GAGTGCATCTTACCATGTACTTTGTCTGTAGTTTCATCAAGAGAGAAAAAG	831
Db	802	GAGTGCATCTTACCATGTACTTTGTCTGTAGTTTCATCAAGAGAGAAAAAG	852

RESULT 12
 US-09-981-915A-96
 ; Sequence 96, Application US/09981915A
 ; Publication No. US20030054986A1
 ; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James;
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2630PIC12
 ; CURRENT APPLICATION NUMBER: US/09/981,915A
 ; CURRENT FILING DATE: 2001-10-16
 ; PRIOR APPLICATION NUMBER: 09/918585
 ; PRIOR FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
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 / PRIOR FILING DATE: 1998-04-21
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 / PRIOR FILING DATE: 1998-05-15
 / PRIOR APPLICATION NUMBER: 60/085704
 / PRIOR FILING DATE: 1998-05-15
 / PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.4%; Score 826.2; DB 10; Length 1016;
 Best Local Similarity 99.6%; Pred. No. 5.7e-258;
 Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	1	ATGAATGGCTTTGCATCCTCTTTCGAGAGAACCAATTTATCTCTCGTGGTACTATTTCCT	60
Db	22	ATGAATGGCTTTGCATCCTCTTTCGAGAGAACCAATTTATCTCTCGTGGTACTATTTCCT	81
QY	61	TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGCTCTACCGCTGAAGTCTGTGCC	120
Db	82	TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGCTCTACCGCTGAAGTCTGTGCC	141
QY	121	ACACACACAATTTCCACGAGACCCAAAGGAGATGATGTTGAAAAGGAGATCCAGAGAA	180
Db	142	ACACACACAATTTCCACGAGACCCAAAGGAGATGATGTTGAAAAGGAGATCCAGAGAA	201
QY	181	GAGGGAAGCATGGCAAGTGGGACGATGGGGCCGAAAGGAATTTAAAGGAGAACTGGGT	240
Db	202	GAGGGAAGCATGGCAAGTGGGACGATGGGGCCGAAAGGAATTTAAAGGAGAACTGGGT	261
QY	241	GATATGGGAGATCGGGCAATATTGGCAAGTCTGGGCCCATTTGGGAGAGAGGTGACAA	300

Db 262 GATATGGAGATCAGGCAATATGCAAGATCTGGCCCATTTGGGAAGAGGGTGCACAA 321
Qy 301 GGGGAAAAAGTTTGTCTTGAATACCTCGAGAAAAGGCAAGCAGGTACTGTCTGTGAT 360
Db 322 GGGGAAAAAGTTTGTCTTGAATACCTCGAGAAAAGGCAAGCAGGTACTGTCTGTGAT 381
Qy 361 TGTGGAAGATACCGGAATTTGTGGAACCTGGAATTTAGTAATGTCCTGGCTCAAGACA 420
Db 382 TGTGGAAGATACCGGAATTTGTGGAACCTGGAATTTAGTAATGTCCTGGCTCAAGACA 441
Qy 421 TCTATGAAGTTTCTCAAGATGTGATGACGAGATTTAGGGAACCTGAAGAGAAATCTTAC 480
Db 442 TCTATGAAGTTTCTCAAGATGTGATGACGAGATTTAGGGAACCTGAAGAGAAATCTTAC 501
Qy 481 TACATGTCGAGAGAGAGAACTACAGGGAATCCCTAAACCACTGACGAGATTCGGGT 540
Db 502 TACATGTCGAGAGAGAGAACTACAGGGAATCCCTAAACCACTGACGAGATTCGGGT 561
Qy 541 GGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACACACTATGCTGCTGATGTTGCC 600
Db 562 GGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACACACTATGCTGCTGATGTTGCC 621
Qy 601 AGAGTGGCTCTTTTGGGTGTTCAATGCGGTGAATGACCTTGAAGGGAGGGACAGTAC 660
Db 622 AGAGTGGCTCTTTTGGGTGTTCAATGCGGTGAATGACCTTGAAGGGAGGGACAGTAC 681
Qy 661 ATGTTCCACAGACACACTCCACTGAGACATATAGCACTGGAATGAGGGGAGCCAGC 720
Db 682 ATGTTCCACAGACACACTCCACTGAGACATATAGCACTGGAATGAGGGGAGCCAGC 741
Qy 721 GACCCCTATGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACA 780
Db 742 GACCCCTATGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACA 801
Qy 781 GAGTGCATCTTACCATGTACTTGTCTGTGATGTCATCAAGAGAAAAAG 831
Db 802 GAGTGCATCTTACCATGTACTTGTCTGTGATGTCATCAAGAGAAAAAG 852

RESULT 13

US-09-978-824-96
; Sequence 96, Application US/09978824
; Publication No. US20030055216A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC14
; CURRENT APPLICATION NUMBER: US/09/978,824
; CURRENT FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
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/ PRIOR APPLICATION NUMBER: 60/085580
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085573
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085704
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.4%; Score 826.2; DB 10; Length 1016;
Best Local Similarity 99.6%; Pred. No. 5.7e-258;
Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGAATGGCTTTGCATCCTTCCTCGAAGAAACCAATTTATCTCTGGTACTATTCTTT 60
DB 22 ATGAATGGCTTTGCATCCTTCCTCGAAGAAACCAATTTATCTCTGGTACTATTCTTT 81
QY 61 TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCGGTCTCTACCGCTGAAGTCTGTGCC 120
DB 82 TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCGGTCTCTACCGCTGAAGTCTGTGCC 141
QY 121 ACACACAAATTTACACAGGACCCAAAGAGATGATGGTGAAGAAAGAGATCCAGAGAA 180
DB 142 ACACACAAATTTACACAGGACCCAAAGAGATGATGGTGAAGAAAGAGATCCAGAGAA 201
QY 181 GAGGAAAGCATGGCAAGTGGGACCGATGGGCGGAAAGGAATTTAAAGGAGAACTGGGT 240
DB 202 GAGGAAAGCATGGCAAGTGGGACCGATGGGCGGAAAGGAATTTAAAGGAGAACTGGGT 261
QY 241 GATATGGGAGATCGGGGCAATTTGGCAAGACTGGGCGCCATTGGGAAGAGAGGTGACAAA 300
DB 262 GATATGGGAGATCAGGGCAATTTGGCAAGACTGGGCGCCATTGGGAAGAGAGGTGACAAA 321
QY 301 GGGGAAAGGTTTGTCTTGGAAATACCTGGGAAAGGCAAGCAGGTACTGTCTGTGAT 360
DB 322 GGGGAAAGGTTTGTCTTGGAAATACCTGGGAAAGGCAAGCAGGTACTGTCTGTGAT 381
QY 361 TGTGAAAGATACCGGAAATTTTGTGGCAAACTGGATATTAGTATTGCCCGGCTCAGACA 420
DB 382 TGTGAAAGATACCGGAAATTTTGTGGCAAACTGGATATTAGTATTGCCCGGCTCAGACA 441
QY 421 TCTATGAAGTTTGTCAAGATGTGATAGCGGATTTAGGAAACTAGAGAAATTTCTAC 480
DB 442 TCTATGAAGTTTGTCAAGATGTGATAGCGGATTTAGGAAACTAGAGAAATTTCTAC 501
QY 481 TACATCGTCAGGAAGAGAACTTACAGGAATTCCTAAACCCACTCAGGATTCGGGGT 540
DB 502 TACATCGTCAGGAAGAGAACTTACAGGAATTCCTAAACCCACTCAGGATTCGGGGT 561
QY 541 GGAATGCTAGCCATGCCCAAGGATGAGCTGCCAACACACTCATCGCTGACTATTGTGCC 600
DB 562 GGAATGCTAGCCATGCCCAAGGATGAGCTGCCAACACACTCATCGCTGACTATTGTGCC 621
QY 601 AAGAGTGGCTTCTTTTCGGGTGTTCATTGGCTGTAATGACCTTTGAAAGGGGAGGACATAC 660
DB 622 AAGAGTGGCTTCTTTTCGGGTGTTCATTGGCTGTAATGACCTTTGAAAGGGGAGGACATAC 681
QY 661 ATGTTCACAGACAACTCCACTGCAGAACTATTAGCACTGGAATGAGGGGGAACCCAGC 720

Db 682 ATGTCCACACACACACTCCTCCTGCGACATATAGCACTTGAATGAGGGGAAACCCAGC 741
QY 721 GACCCCTATGCTATGAGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACA 780
Db 742 GACCCCTATGCTATGAGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACA 801
QY 781 GAGTGCCATCTTACCATTGCTTGTCTGTGAGTTTCATCAAGAGAAAAG 831
Db 802 GAGTGCCATCTTACCATTGCTTGTCTGTGAGTTTCATCAAGAGAAAAG 852

RESULT 14

US-09-918-585A-96
Sequence 96, Application US/09918585A
Publication No. US20030060406A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C1
CURRENT APPLICATION NUMBER: US/09/918,585A
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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 PRIOR APPLICATION NUMBER: 60/085697
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/086023

Query Match 99.4%; Score 826.2; DB 10; Length 1016;
 Best Local Similarity 99.6%; Pred. No. 5.7e-258;
 Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	1	ATGAATGCGCTTTGGATCCTCTGCTTGAAGAAACCAATTTATCTCTCTGCTACTATTTCTT	60
Db	22	ATGAATGCGCTTTGGATCCTCTGCTTGAAGAAACCAATTTATCTCTCTGCTACTATTTCTT	81
Qy	61	TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGCTCTACCGCTGGAAGTCTGTGCC	120
Db	82	TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGCTCTACCGCTGGAAGTCTGTGCC	141
Qy	121	ACACACAAATTTCCAGAGCCCAAGAGGATGATGGTGAAGAGGAGATCCAGGAGAA	180
Db	142	ACACACAAATTTCCAGAGCCCAAGAGGATGATGGTGAAGAGGAGATCCAGGAGAA	201
Qy	181	GAGGGAAGCATGGCAAAAGTGGACCGCATGGGCGCAAGATTTAAAGGAGAACTCGGT	240
Db	202	GAGGGAAGCATGGCAAAAGTGGACCGCATGGGCGCAAGATTTAAAGGAGAACTCGGT	261
Qy	241	GATATGGGAGATCGGGGCAATTTTGGCAAGTCTGGGCCCATTTGGGAAGAGGATGACAAA	300
Db	262	GATATGGGAGATCAGGGCAATTTTGGCAAGTCTGGGCCCATTTGGGAAGAGGATGACAAA	321
Qy	301	GCGGAAAAAGTTTCTTGGATACCTCGAGAAAAAGCAAGCAGGTACTGTCTGTGAT	360
Db	322	GCGGAAAAAGTTTCTTGGATACCTCGAGAAAAAGCAAGCAGGTACTGTCTGTGAT	381
Qy	361	TGTGGAAGATACCGGAAATTTTGTGGCAAACTGGATATTAGTATTTGCCCGGCTCAAGACA	420
Db	382	TGTGGAAGATACCGGAAATTTTGTGGCAAACTGGATATTAGTATTTGCCCGGCTCAAGACA	441
Qy	421	TCTATGAAGTTTGTCAAGATGTGATAGCAGGATTTAGGGAACTGGAAGAAATTTCTAC	480
Db	442	TCTATGAAGTTTGTCAAGATGTGATAGCAGGATTTAGGGAACTGGAAGAAATTTCTAC	501
Qy	481	TACATCGTCCAGGAAGAGAACTACAGGGAACTCCCTAACCCCTGCGAGGATTCGGGGT	540
Db	502	TACATCGTCCAGGAAGAGAACTACAGGGAACTCCCTAACCCCTGCGAGGATTCGGGGT	561
Qy	541	GGAATGCTAGCCATGCCCAAGGATGAAGTGCACACACACTCATCGCTGACTATGTGTGCC	600
Db	562	GGAATGCTAGCCATGCCCAAGGATGAAGTGCACACACACTCATCGCTGACTATGTGTGCC	621
Qy	601	AAGAGTGGCTTTCTTTGGGTGTTTCTTGGCGTGAATGACCTTGAAGAGGAGGACAGTAC	660
Db	622	AAGAGTGGCTTTCTTTGGGTGTTTCTTGGCGTGAATGACCTTGAAGAGGAGGACAGTAC	681
Qy	661	ATGTTCAACAGACACACTCCACTGAGAACTATAGCAACTGGAATGAGGGGAAACCCAGC	720
Db	682	ATGTTCAACAGACACACTCCACTGAGAACTATAGCAACTGGAATGAGGGGAAACCCAGC	741
Qy	721	GACCCCTATGCTCATGAGGACTGTGTGAGATGCTGAGCTCTGGCAGATGGAATGACACA	780
Db	742	GACCCCTATGCTCATGAGGACTGTGTGAGATGCTGAGCTCTGGCAGATGGAATGACACA	801
Qy	781	GAGTGGCAATCTTACCATGACTTTTGTGTGATTTCTGATTCATCAGAGAGAAAG	831
Db	802	GAGTGGCAATCTTACCATGACTTTTGTGTGATTTCTGATTCATCAGAGAGAAAG	852

RESULT 15
 US-09-978-423A-96
 ; Sequence 96, Application US/09978423A
 ; Publication No. US20030069178A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Deanyers, Luc
 ; APPLICANT: Eacon, Dan
 ; APPLICANT: Ferrari, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
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APPLICANT: Gurney, Austin L.
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APPLICANT: Kijavini, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C21
CURRENT APPLICATION NUMBER: US/09/978,423A
CURRENT FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: 09/918595
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
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PRIOR APPLICATION NUMBER: 60/066364
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PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
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PRIOR FILING DATE: 1998-03-31
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PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
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PRIOR FILING DATE: 1998-04-27
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PRIOR APPLICATION NUMBER: 60/083392
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PRIOR APPLICATION NUMBER: 60/083499
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PRIOR APPLICATION NUMBER: 60/083558
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PRIOR APPLICATION NUMBER: 60/083559
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083500
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083742
PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366

;; PRIOR FILING DATE: 1998-05-05
;; PRIOR APPLICATION NUMBER: 60/084414
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;; PRIOR APPLICATION NUMBER: 60/084441
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;; PRIOR APPLICATION NUMBER: 60/084640
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084598
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;; PRIOR APPLICATION NUMBER: 60/084600
;; PRIOR FILING DATE: 1998-05-07
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;; PRIOR APPLICATION NUMBER: 60/085339
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;; PRIOR APPLICATION NUMBER: 60/085338
;; PRIOR FILING DATE: 1998-05-13
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;; PRIOR APPLICATION NUMBER: 60/085582
;; PRIOR FILING DATE: 1998-05-15
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;; PRIOR APPLICATION NUMBER: 60/085689
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085579
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085580
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085573
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.4%; Score 826.2; DB 10; Length 1016;

Best Local Similarity 99.6%; Pred. No. 5.7e-258;

Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	1	ATGAATGGCTTTGCTTCCTTCGAGAAACCAATTTATCCTCTGTGACTATTCTT	60
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Qy	61	TTGCAAAATTCAGAGCTGGGCTCTGGATATTGATAGCCGCTCTACCGCTGAAGTCTGTGCC	120
Db	82	TTGCAAAATTCAGAGCTGGGCTCTGGATATTGATAGCCGCTCTACCGCTGAAGTCTGTGCC	141
Qy	121	ACACACAAATTTCCAGACCCCAAGAGATGATGGTGAAAGAGAGATCCAGAGAA	180
Db	142	ACACACAAATTTCCAGACCCCAAGAGATGATGGTGAAAGAGAGATCCAGAGAA	201
Qy	181	GAGGGAAGCATGGCAAGTGGGACGATGGGGCCGAAAGGAATTAAGAGAACTGGGT	240
Db	202	GAGGGAAGCATGGCAAGTGGGACGATGGGGCCGAAAGGAATTAAGAGAACTGGGT	261
Qy	241	GATATGGGAGATCGGGCAATATTGGCAAGATCTGGGCCCATTTGGGAAGAGGGTGACAAA	300
Db	262	GATATGGGAGATCAGGGCAATATTGGCAAGATCTGGGGCCCATTTGGGAAGAGGGTGACAAA	321
Qy	301	GGGGAAGAGGTTTGTGGAATACCTGGAGAAAAGGCAAGGAGGAGTACTGTCTGTGAT	360
Db	322	GGGGAAGAGGTTTGTGGAATACCTGGAGAAAAGGCAAGGAGGAGTACTGTCTGTGAT	381
Qy	361	TGTGGAAGATACCGAAATTTGTGGCAACTGGATATTAGTATTGCCGGCTCAAGACA	420
Db	382	TGTGGAAGATACCGAAATTTGTGGCAACTGGATATTAGTATTGCCGGCTCAAGACA	441

Qy	421	TCATGAAGTTTGTCAAGAAATGTGATAGCAGGGATTAGGGAACCTGAAGAGAAATTTCTAC	480
Db	442	TCATGAAGTTTGTCAAGAAATGTGATAGCAGGGATTAGGGAACCTGAAGAGAAATTTCTAC	501
Qy	481	TACATCGTGCAGGAAGAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGGGGT	540
Db	502	TACATCGTGCAGGAAGAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGGGGT	561
Qy	541	GGAATGCTAGCCATGCCCAAGGATGAAGTGCACACACACTCATCGCTGACTATTGTGCC	600
Db	562	GGAATGCTAGCCATGCCCAAGGATGAAGTGCACACACACTCATCGCTGACTATTGTGCC	621
Qy	601	AAGAGTGGCTTCTTTCCGGGTGTTTCATTGGCGTGAATGACCTTGAAGGAGGACAGTAC	660
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Qy	661	ATGTTCAACAGAACCACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGAAACCCAGC	720
Db	682	ATGTTCAACAGAACCACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGAAACCCAGC	741
Qy	721	GACCCCTATGGTCAAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACACA	780
Db	742	GACCCCTATGGTCAAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACACA	801
Qy	781	GAGTGGCACTTTACCATGTAATTTGTGTGTGAGTTTCATCAAGAGAAAAAG	831
Db	802	GAGTGGCACTTTACCATGTAATTTGTGTGTGAGTTTCATCAAGAGAAAAAG	852

Search completed: March 11, 2004, 18:42:46

Job time : 373 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 16:44:12 ; Search time 2531 Seconds

(without alignments)
9804.612 Million cell updates/sec

Title: US-09-600-932-1_COPY_6_836

Perfect score: 831

Sequence: 1 atgaatggcttgcacacctt.....agttcatcaagaagaaaag 831

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estnu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pin:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_nam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	827.8	99.6	834	29	AY409410 Homo sapi
2	823	99.0	834	29	AY409411 Pan trogl
3	669.6	80.5	752	12	BM009998 603630745
4	644.4	77.5	4591	11	AK028423 Mus muscu

5	642.8	77.4	834	29	AY409412	Mus muscu
6	462.8	55.7	560	13	EX494095	DRF2p779A
7	455	54.8	955	10	BB612129	BB612129
8	444.4	53.5	609	12	BM010788	603629302
9	427.8	51.5	457	13	EX496500	EX496500
10	409.2	49.2	492	10	BF078010	228226 MA
11	392.8	47.3	930	14	CF378429	AGENCOURT
12	389.6	46.9	747	14	CB228545	AGENCOURT
13	386	46.5	499	12	BI457460	389071 MA
14	308.4	37.1	636	13	EX671934	EX671934
15	302.6	36.4	654	12	BI067078	pglin.pk0
16	297	35.7	890	14	CF378456	AGENCOURT
17	274.8	33.1	380	10	BB869893	BB869893
18	273.6	32.9	354	10	AW435866	75149 MAR
19	268.6	32.3	1239	12	BM551435	AGENCOURT
20	265.4	31.9	361	10	BB869996	BB869996
21	255.2	30.7	325	13	BY332718	BY332718
22	251	30.2	743	13	SU290748	603608166
23	249	30.0	451	10	AW355638	pf11c.pk0
24	241.6	29.1	486	12	BM426695	pgf2n.pk0
25	239.6	28.8	344	13	BY008444	BY008444
26	239	28.8	1383	11	AK003121	Mus muscu
27	238	28.6	326	14	R29493	F1-1006D 22
28	235.8	28.4	1201	13	EX427124	EX427124
29	229	27.6	894	13	SU147034	AGENCOURT
30	218.2	26.3	1143	13	EX333394	EX333394
31	201	24.2	362	14	R97480	YQ53102.r1
32	197.4	23.8	670	14	CB141360	K-ESTO194
33	190.6	22.9	1132	13	EX394893	EX394893
34	188.6	22.7	324	13	BY331120	BY331120
35	184.6	22.2	1201	13	EX394625	EX394625
36	184.4	22.2	1201	13	EX394624	EX394624
37	180	21.7	734	14	CB430533	CB430533
38	179	21.5	962	13	BQ927000	AGENCOURT
39	174.2	21.0	505	14	CB418352	591149 NA
40	172.6	20.8	962	13	BQ69775	AGENCOURT
41	172.4	20.7	893	10	BF314316	601901046
42	169.4	20.4	610	14	CB056003	CB056003
43	162.8	19.6	569	29	CE798050	NIISC_jj11
44	161	19.4	590	9	AV690347	tigr-gss-
45	157.2	18.9	645	13	BU404074	604136366

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION Homo sapiens COLEC10 gene, VIRTUAL TRANSCRIPT, partial sequence,
834 bp DNA linear GSS 16-DEC-2003
AY409410
Genomic survey sequence.
ACCESSION AY409410.1 GI:39765378
VERSION AY409410.1
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 834)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL
Science 302 (5652), 1960-1963 (2003)
PUBMED
14671302
REFERENCE
2 (bases 1 to 834)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE
Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES

source 1..834
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
<1..834
/gene="COLEC10"
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gene

ORIGIN

Query Match 99.6%; Score 827.8; DB 29; Length 834;
Best Local Similarity 99.8%; Pred. No. 18-217; Indels 0; Gaps 0;
Matches 829; Conservative 0; Mismatches 2;

Qy 1 ATGAATGGCTTTCACCTCTGCTTTCGAAGAACCAATTTATCTCTCTGCTACTATTTCTT 60
Db 1 ATGAATGGCTTTCACCTCTGCTTTCGAAGAACCAATTTATCTCTCTGCTACTATTTCTT 60

Qy 61 TTGCAATTCAGAGTCGGTCTGGATATGATAGCCGCTTACCGCTGAAGTCTGTGCC 120
Db 61 TTGCAATTCAGAGTCGGTCTGGATATGATAGCCGCTTACCGCTGAAGTCTGTGCC 120

Qy 121 ACACACAAATTTACACAGACCCCAAGAGAGATGATGTGAAAAAGAGAGATCCAGAGAA 180
Db 121 ACACACAAATTTACACAGACCCCAAGAGAGATGATGTGAAAAAGAGAGATCCAGAGAA 180

Qy 181 GAGGAAAGCATGCGAAATGGGACCCATCGGCGCGAAGAGAAATTAAGAGAACTGGGT 240
Db 181 GAGGAAAGCATGCGAAATGGGACCCATCGGCGCGAAGAGAAATTAAGAGAACTGGGT 240

Qy 241 GATATGGAGATCGGGCAATATTTGGCAAGACTGGGCCCATTTGGGAAGAGAGGATCCAGAGAA 300
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Qy 301 GGGGAAAAGGTTTGGTGAATACCTGAGAAAAAGGCAAGAGGATCTGTCTGTGAT 360
Db 301 GGGGAAAAGGTTTGGTGAATACCTGAGAAAAAGGCAAGAGGATCTGTCTGTGAT 360

Qy 361 TGTGGAAGTACCGGAAATTTGTTGCACTGGATATTAGTATTCGCCGCTCAAGACA 420
Db 361 TGTGGAAGTACCGGAAATTTGTTGCACTGGATATTAGTATTCGCCGCTCAAGACA 420

RESULT 2
AY409411 834 bp DNA linear GSS 16-DEC-2003
LOCUS Pan troglodytes COLEC10 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY409411
VERSION AY409411.1 GI:39765379
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
REFERENCE 1 (bases 1 to 834)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 834)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES
source 1..834
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1..834
/gene="COLEC10"
/locus_tag="HCM3548"

ORIGIN

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Best Local Similarity 99.4%; Pred. No. 2-216; Indels 0; Gaps 0;
Matches 826; Conservative 0; Mismatches 5;

Qy 1 ATGAATGGCTTTCACCTCTGCTTTCGAAGAACCAATTTATCTCTCTGCTACTATTTCTT 60
Db 1 ATGAATGGCTTTCACCTCTGCTTTCGAAGAACCAATTTATCTCTCTGCTACTATTTCTT 60

Qy 61 TTGCAATTCAGAGTCGGTCTGGATATGATAGCCGCTTACCGCTGAAGTCTGTGCC 120
Db 61 TTGCAATTCAGAGTCGGTCTGGATATGATAGCCGCTTACCGCTGAAGTCTGTGCC 120

Qy 121 ACACACAAATTTACACAGACCCCAAGAGAGATGATGTGAAAAAGAGATCCAGAGAA 180
Db 121 ACACACAAATTTACACAGACCCCAAGAGAGATGATGTGAAAAAGAGATCCAGAGAA 180

Qy 181 GAGGAAAGCATGCGAAATGGGACCCATCGGCGCGAAGAGAAATTAAGAGAGACTGGGT 240
Db 181 GAGGAAAGCATGCGAAATGGGACCCATCGGCGCGAAGAGAAATTAAGAGAGACTGGGT 240

Qy 241 GATATGGAGATCGGGCAATATTTGGCAAGACTGGGCCCATTTGGGAAGAGAGGATCCAGAGAA 300
Db 241 GATATGGAGATCGGGCAATATTTGGCAAGACTGGGCCCATTTGGGAAGAGAGGATCCAGAGAA 300

Qy 301 GGGGAAAAGGTTTGGTGAATACCTGAGAAAAAGGCAAGAGGATCTGTCTGTGAT 360
Db 301 GGGGAAAAGGTTTGGTGAATACCTGAGAAAAAGGCAAGAGGATCTGTCTGTGAT 360

Qy 361 TGTGGAAGTACCGGAAATTTGTTGCACTGGATATTAGTATTCGCCGCTCAAGACA 420
Db 361 TGTGGAAGTACCGGAAATTTGTTGCACTGGATATTAGTATTCGCCGCTCAAGACA 420

AKO28423	Mus musculus	14 days embryo liver cDNA, RIKEN full-length enriched library; clone:4432404O08 product:COLLECTIN 34 homolog [Homo sapiens], full insert sequence.	4591 bp	mRNA	linear	HTC 18-SEP-2003
ACCESSION	AKO28423					
VERSION	AKO28423.1	GI:26324373				
KEYWORDS	HTC; CAP trapper.					
SOURCE	Mus musculus (house mouse)					
ORGANISM	Mus musculus					
REFERENCE	Eukaryota; Metazoa; Chordata; Cranita; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.					
AUTHORS	Carninci,P. and Hayashizaki,Y.					
TITLE	High-efficiency full-length cDNA cloning					

RESULTS 4
 LOCUS AKO28423
 DEFINITION Mus musculus 14 days embryo liver cDNA, RIKEN full-length enriched library, clone:4432404O08 product:COLLECTIN 34 homolog [Homo sapiens], full insert sequence.
 ACCESSION AKO28423
 VERSION AKO28423.1 GI:26324373
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 REFERENCE 1
 AUTHORS Carninci, P. and Hayashizaki, Y.
 TITLE High-efficiency full-length cDNA cloning


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Db      727 GACCCCTCCGGCCATGAGGACTGTGTGGAGATGTTGAGCTCTGGCAGGTGGAATGACACA 786
QY      781 GAGTGCCATCTTACCATGACTTCTGCTGAGTTCATCAAGAGAAAA 830
Db      787 GAGTGCCATCTTACCATGACTTCTGCTGAGTTCATCAAGAGAAAA 836

RESULT 5
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LOCUS      Mus musculus COLEC10 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION      genomic survey sequence.
ACCESSION      AY409412
VERSION      AY409412.1 GI:39765380
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
REFERENCE      Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 834)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE      Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL      Science 302 (5652), 1960-1963 (2003)
PUBMED      14671302
REFERENCE      2 (bases 1 to 834)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE      Direct Submission
JOURNAL      Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT      This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES      Location/Qualifiers
source      1..834
             /organism="Mus musculus"
             /mol_type="genomic DNA"
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             /gene="COLEC10"
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ORIGIN
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Best Local Similarity 85.9%; Pred. No. 1.6e-166;
Matches 713; Conservative 0; Mismatches 117; Indels 0; Gaps 0;
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Db      1 ATGAATGGCTTTAGAGTCTCTGCTTCAAGCAACCTATCCATGCTGTGCTGCTAGCTTC 60
QY      61 TTGCMAATTCAGAGTCTGGTCTGATATTGATAGCCCTCTCAACGCTGAAGTCTGGCC 120
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Db      121 ACACATACATTCACAGACCTTAAGGGATGATGTTGAAGAGTGACACAGAGAA 180
QY      181 GAGGGAACATCGGCAATGCGGACCGCTGCGGCCGGAAGGAATTAAGGAGAACTGGGT 240
Db      181 GAAGGCAAGATGGCAAGTGGGACCGCCAGGAGCAAAAGAGTGAAGGAGAGCTGGGT 240
QY      241 GATATGGGAGATCGGGCAATATTGGCAAGACTGGGCCCATTTGGAGAGAGGGTGACAA 300
Db      241 GATATGGGAGCCAGGGAATATTGGCAAGTGTGGCCCTATTCGCAAGAGAGGGTGACAA 300
QY      301 GGGGAAAAAGTTTGTCTTGGATACCTGGAGAAAAAGCAAGCAGGTACTGTCTGTGAT 360

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Db      301 GGGGAAAAAGGTCTGCTTGGATTTCTTGGAGAAAAAGCAAGCAGGTACTGTGTGAT 360
QY      361 TGTGGAAGATACCGGAAATTTGTTGGCAACTGGATATTAGTATTGCCCGCTCAAGACA 420
Db      361 TGTGCGAGGTACCGGAAAGTGGTTGGCAACTGGATATTAGTATTGCTCTCTTAAGACA 420
QY      421 TCTATGAAGTTTGTCAAGAATGTGATAGCAGGGATTAGGGAAAACTGAAGAGAAATTTCTAC 480
Db      421 TCAATGAATTCATCAAGAATGTTATAGCAGGGATCCGGGAAACTGAAGAGAAATTTCTAC 480
QY      481 TACATCGTGCAGGAGAGAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGGGT 540
Db      481 TACATTTGTCAGGAGGAGAGAACTACAGGGAATCTCTGACCCACTGCAGGATCCGAGGA 540
QY      541 GGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACACACTCATCGTGAATATGTTGCC 600
Db      541 GGGATGCTAGCCATGCCCAAGGATGAAGCTGTTAACHACCCCTTATTTGCTGATATGTCGCC 600
QY      601 AAGAGTGGCTTCTTTCGGGTGTTTCATTTGGCGTGAATGACCTTGAAGAGGGAGGACAGTAC 660
Db      601 AAGAGTGGTCTTCTTTCAGAGTGTTCATTTGGGTCAATGACCTTGAGAGGGAGGGCAATAT 660
QY      661 ATGTTACAGACAACTCTCCACTGCAGAACTATAGCAACTGGAACTGAGGGGGAACCCAGC 720
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QY      721 GACCCCTATGTCATGAGGACTGTGTGAGATGCTGAGCTCTGGCAGATGGAATGACACA 780
Db      721 GACCCCTCCGCCCATGAGGACTGTGTGAGATGCTGAGCTCTGGCAGATGGAATGACACA 780
QY      781 GAGTGCCATCTTACCATGACTTCTGCTGAGTTCATCAAGAGAAAAA 830
Db      781 GAGTGTCACCTTACCATGATTTTGTCTGTGATTTGTCAGAGAAAAA 830

RESULT 6
BX494095      560 bp mRNA linear EST 04-SEP-2003
LOCUS      DKFZp779A1511.k1.779 (synonym: hnccl) Homo sapiens cDNA clone
DEFINITION      DKFZp779A1511.5, mRNA sequence.
ACCESSION      BX494095
VERSION      BX494095.1 GI:32007261
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Wambutt,R., Heubner,D., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
Fobo,G., Han,M. and Wiemann,S.
EST (Wambutt,R., Heubner,D., Mewes,H.W., Weil,B., Amid,C., et al.)
Unpublished (2003)
Contact: MIPS
MIPS      Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
consortium of the German Genome Project.
No sl sequence available.
This clone (DKFZp779A1511) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
location/Qualifiers
1..560
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp779A1511"
/tissue_type="liver"
/dev_stage="fetal"
FEATURES      source

```

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. *Genome Res.* 10 (10), 1617-1630 (2000)

wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. *Genome Res.* 10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001)

Yamanaka, I., Kiyosawa, H., Kondo, S., Saito, T., Shinagawa, A., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., Arakawa, T., Ishii, Y. and Hayashizaki, Y.

Mapping of 19032 mouse cDNAs on mouse chromosomes. *J. Struct. Func. Genomics* 2 pre, L72-L96 (2001)

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

e mouse tissues.

Location/Qualifiers

1. 955

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="4432404008"

/sex="mixed"

/tissue_type="liver"

/dev_stage="P14 days embryo"

/lab_host="DH10B"

/clone_lib="RIKEN full-length enriched, 14 days embryo liver"

/notes="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAAGATCCAGAGCTCTTTTCTTTTCTTTTCTT 3'], cDNA was prepared by using trihalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATCTCGAGTAAATTAATCCCTCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I"

ch 54.8%; Score 455; DB 10; Length 955;

Similarity 81.3%; Pred. No. 1.6e-114;

337; Conservative 0; Mismatches 116; Indels 3; Gaps 1;

1 1 ATGAATGCTTTGATCCTCTTGTTCGAGAAACCAATTTATCTCTCTGGTACTATTTCTT 60

9 9 ATGAATGCTTTGAGTCTTGTTCGAGAACCACTATCAATGCTGTTGCTGCTAGCTCTC 68

51 TTGCAAAATTCAGAGCTCTGGGCTCTGGATATTGATAGCGCTCTTACCGCTGAAGTCTGTGCC 120

59 TTGCATTTTCAGAGCTCTGGGCTCTGGATTTGATAGTCATCAGTCTGCAAGTCTGTGCC 128

11 ACACACATTTTACACAGAACCAAGAGGATGTGGTGAAGAGGAGGATCCAGGAGAA 180

59 ACACATCAATTTTACACAGAACCTAAGGGGATGTGGTGAAGAGGAGGATCCAGGAGAA 188

181	QY	GAGGGAAGCATGGCAAAAGTGGAGCGCATGGGGCCGAAAGGAATTTAAAGGAACTGGGT	240
189	Db	GAAGGCAAGGATGGCAAAAGTGGAGCGCCAGGGACCAAAGGAGTGAAGAGAGCTGGT	248
241	QY	GATATGGGAGATCGGGGCAATATTGGCAAGACTGGGCCCATTCGGGAAGAAGGGTGCACAA	300
249	Db	GATATGGGAGCCGAGGTTAATTATTGGCAGTCTGGCCCTATTGGCAAGAAGGGTGCACAA	308
301	QY	GGGGAAAAGGTTTGTCTTGGGAATACCTTGGAGAAAAGGCCAAAGCAAGGTACTGTCTGTGAT	360
309	Db	GGGGAAAAGGGTCTGTCTTGGGAATTCCTTGGAGAAAAGGCCAAAGCAGGTACCATCTGTGAT	368
361	QY	TGTGGAAAGATACCGGAAATTTGTGGCAACTGGAATTAGTATTGTCCCGCGCTCAAGCA	420
369	Db	TGTGGCAGGTACCGGAAGTGTGGAAACTGGAATTAGTATTGTCTCGTCTTTAAGACA	428
421	QY	TCTATGAAGTTTGTCAAGANTGTCATAGCAGGATTAGGGAAACTGAAGAGAAATTTCTAC	480
429	Db	TCAATGAAATTCATCAAGAATGTTATAGCAGGATCCGGGAACTGAAGAGAAATTTCTAC	488
481	QY	TACATCGTGCAGGAGAGAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGGGGT	540
489	Db	TACATTGTGCAGGAGGAGAAACTACAGGGAATCTCTGACCCATCTGCAGGATCCGAGGA	548
541	QY	GGAAATGCTAGCCATGCCCCAAGGATGAAGCTGCCAACACACTCATCGCTCACTATGTTGCC	600
549	Db	GGAGTCTAGCCATGCTCAGAGATGAAGTGTGTGACACCCCTTATTGCTGACTAATGTGCCC	608
601	QY	AAGAGTGGCTTCTTTTCGGGTCTTCATTGGCGTGAATGACCTTTGAAAGGAGGGAACA	656
609	Db	---AGAGTGGTTCTTCAGAGTGTTCATATGGGGTCATTACTTTGAGAGGNGGGGCA	661

RESULT 8					
BM010788					
LOCUS	BM010788	609 bp	mrna	linear	EST 30-OCT-2001
DEFINITION	503829302F1 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5434680 5', mrna sequence.				

FEATURES	SOURCE
1. Feature 1	Source 1
2. Feature 2	Source 2
3. Feature 3	Source 3
4. Feature 4	Source 4
5. Feature 5	Source 5
6. Feature 6	Source 6
7. Feature 7	Source 7
8. Feature 8	Source 8
9. Feature 9	Source 9
10. Feature 10	Source 10

RESULT 9	
BX496500	
LOCUS	457 bp mRNA linear EST 04-SEP-2003
DEFINITION	DKFZp779M0527_r1.779 (synonym: hnccl) Homo sapiens cDNA clone
ACCESSION	DKFZp779M0527_5, mRNA sequence.
VERSION	
KEYWORDS	
SOURCE	EST.
ORGANISM	Homo sapiens (human)
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 457) Koehler,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.
TITLE	EST (Koehler,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., et al.)
JOURNAL	Unpublished (2003)
COMMENT	Contact: MIPS MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by BMFZ (Biomedical Research Center at the Heinrich-Heine-University, Duesseldorf/Germany) within the cDNA sequencing consortium of the German Genome Project. No s1 sequence available. This clone (DKFZp779M0527) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES	Location/Qualifiers

FEATURES

source

1. .457
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="DKF2p779M0527"
 /tissue_type="liver"
 /dev_stage="fetal"
 /lab_host="DH10B"
 /notes="Vector: pSport1_Sfi; Site_1: SfiI; Site_2: SfiIb"
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ORIGIN

Query Match 51.5%; Score 427.8; DB 13; Length 457;
 Best Local Similarity 99.5%; Pred. No. 3.9e-107;
 Matches 425; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ATGAATGGCTTCATCTCTGCTTCGAGAAACCAATTTATCTCTCTGCTACTATTTCTT 60
 Db 27 ATGAATGGCTTCATCTCTGCTTCGAGAAACCAATTTATCTCTCTGCTACTATTTCTT 86
 QY 61 TTGCAAAATTCAGAGTCTGGTCTGGATATTGATAGCGCTCTACCGCTGAAGTCTGTGCC 120
 Db 87 TTGCAAAATTCAGAGTCTGGTCTGGATATTGATAGCGCTCTACCGCTGAAGTCTGTGCC 146
 QY 121 ACACACACAAATTTACACAGACCCAAAGAGAGATGATGGTGAAAAAGGAGATCCAGGAAA 180
 Db 147 ACACACACAAATTTACACAGACCCAAAGAGAGATGATGGTGAAAAAGGAGATCCAGGAAA 206
 QY 181 GAGGAAAGCATGGCAAGTGGGACCCATGGGCGGCAAGGAATTAAGGAGAACTGGGT 240
 Db 207 GAGGAAAGCATGGCAAGTGGGACCCATGGGCGGCAAGGAATTAAGGAGAACTGGGT 266
 QY 241 GATATGGAGATCGGGGCAATATTGCAAGACTGGGCCCATTTGGGAAGAGGGTGCACAAA 300
 Db 267 GATATGGAGATCGGGGCAATATTGCAAGACTGGGCCCATTTGGGAAGAGGGTGCACAAA 326
 QY 301 GGGGAAAAAGTTTCTTGAATACCTGGAGAAAAAGGCAAGCAAGTACTGTCTGTGAT 360
 Db 327 GGGGAAAAAGTTTCTTGAATACCTGGAGAAAAAGGCAAGCAAGTACTGTCTGTGAT 386
 QY 361 TGTGGAAGATACCGGAATTTGTTGACAACTGATATTAGTATTCCTCGGCTCAAGACA 420
 Db 387 TGTGGAAGATACCGGAATTTGTTGACAACTGATATTAGTATTCCTCGGCTCAAGACA 446
 QY 421 TCTATGAAGTT 431
 Db 447 TCTATGAAGTT 457

RESULT 10

BF078010 492 bp mRNA linear EST 18-OCT-2000
 LOCUS 228226 MARC 2P1G Sus scrofa cDNA 5', mRNA sequence.
 DEFINITION BF078010
 ACCESSION BF078010.1 GI:10871840
 VERSION EST.
 KEYWORDS Sus scrofa (pig)
 SOURCE Sus scrofa

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 1 (bases 1 to 492)
 Fahrenkrug, S.C., Smith, T.P.L., Preking, B.A., Cho, J., White, J.,
 Vallet, J., Wise, T., Rohrer, G.A., Perlea, G., Sultana, R.,
 Quackenbush, J. and Keele, J.W.

TITLE

Porcine gene discovery by normalized cDNA-library sequencing and

EST cluster assembly

Mamm. Genome 13 (8), 475-478 (2002)

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called and alt trimmed with phred
 v0.980904.e. Vector identified by cross_match with the -minscore 18
 and -minmatch 12 options.

PCR Primers
 FORWARD: AGGAACAGCTATGACCAT
 BACKWARD: GTTTCACAGTCACGAGG
 Plate: 49 row: P column: 11
 Seq primer: ATTAGGTGACACATATAG.

FEATURES

source

1. .492
 /organism="Sus scrofa"
 /mol_type="mRNA"
 /db_xref="taxon:9823"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /clone_lib="MARC 2P1G"
 /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
 library made from pooled tissue from testis, ovary,
 endometrium, hypothalamus, pituitary, and placenta."

ORIGIN

Query Match 49.2%; Score 409.2; DB 10; Length 492;
 Best Local Similarity 90.1%; Pred. No. 5.6e-102;
 Matches 438; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
 QY 1 ATGAATGGCTTTGCACTCTGCTTCGAGAAACCAATTTATCTCTCTGCTACTATTTCTT 60
 Db 7 ATGGGTGGCTCTGGAGCTGGACCTCGAAGAACAGTTTCATCTCTCTGCTTCTTCTT 66
 QY 61 TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCGTCTCTACCGCTGAAGTCTGTGCC 120
 Db 67 TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCGTCTCTACCGCTGAAGTCTGTGCC 126
 QY 121 ACACACACAAATTTACACAGGACCCAAAGAGATGATGGTGAAAAAGGAGATCCAGGAGAA 180
 Db 127 ACACACACAAATTTACACAGGACCCAAAGAGATGATGGTGAAAAAGGAGATCCAGGAGAG 196
 QY 181 GAGGAAAGCATGGCAAGTGGGACCCATTTGGCAAGACTGGGCCCATTTGGGAAGAGGGTGCACAA 300
 Db 187 GAGGAAAGCATGGCAAGTGGGACCCATTTGGCAAGACTGGGCCCATTTGGGAAGAGGGTGCACAA 306
 QY 241 GATATGGAGATCGGGGCAATATTGCAAGACTGGGCCCATTTGGGAAGAGGGTGCACAA 360
 Db 247 GATATGGAGATCGGGGCAATATTGCAAGACTGGGCCCATTTGGGAAGAGGGTGCACAA 366
 QY 301 GGGGAAAAAGGTTTCTTGAATACCTGGAGAAAAAGGCAAGCAAGTACTGTCTGTGAT 420
 Db 361 TGTGGAAGATACCGGAATTTGTTGACAACTGATATTAGTATTCCTCGGCTCAAGACA 426
 QY 421 TCTATGAAGTTTGTCAAGAAATGATAGCAGGGAATTAGGGAAACTGAAGAGAAATTTCTAC 480
 Db 427 TCGATGAAGTTTGTCAAGAAATGATAGCAGGGAATTCGGGAAACCGAAGAGAAATTTCTAC 486
 QY 481 TACATC 486
 Db 487 TACATC 492

RESULT 11

CF378429

LOCUS

DEFINITION

IMAGE:7005528 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

CF378429 930 bp mRNA linear EST 27-AUG-2003
 AGENCOURT_15349559 NICHD_XGC_SwB1N Silurana tropicalis cDNA clone
 IMAGE:7005528 5', mRNA sequence.

CF378429

CF378429.1 GI:34315873

EST.

Silurana tropicalis (western clawed frog)

ORGANISM

Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Silurana.

REFERENCE

NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics

AUTHORS

National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Rob Granger, University of Virginia
cDNA Library Preparation: Open Biosystems

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM14704 row: j column: 22

High quality sequence stop: 677.

FEATURES

source

1. .930

/organism="Silurana tropicalis"

/mol_type="mRNA"

/db_xref="taxon:8364"

/clone="IMAGE:7005528"

/tissue_type="whole body"

/clone_lib="NICHD XGC Swb1N"

/note="Vector: pExpress-1; Site 1: EcoRV; Site 2: NotI;
Bulk tissue was collected from a whole 10 month old male
from the F6 strain. 1st strand cDNA was primed with a Not
I - oligo(dN) primer, double-stranded cDNA was cloned into
the Not I and EcoRV sites of pExpress-1. Library was
size-selected for >1.5 kb fragments for an average insert
size of 1.92 kb. Library was normalized to Cot5 with a
180-fold reduction of actin. A non-normalized version of
this library is also available (NICHD XGC Swb1). Library
was constructed by Open Biosystems (Huntsville, AL)."

ORIGIN

Query Match 47.3%; Score 392.8; DB 14; Length 930;
Best Local Similarity 68.7%; Pred. No. 2.6e-97;
Matches 541; Conservative 0; Mismatches 247; Indels 0; Gaps 0;

QY 44 TCTGTGTAATTTCTTTGCAATTCAGAGCTGGGTCTGATATTGATAGCGGTCTTA 103
DB 102 TCTGTGGGTGATAGCGGTACATGTGCGGCTCTCTTTGGAGGTGAGAACAGTTCTG 161
QY 104 CCGCTGAAGTCTGTGCACACACAAATTCACAGGACCCAAAGGAGATGATGGTGA 163
DB 162 CTGTGATACTTGTTCCTCACTCACCAATTCGCGGGACCCAAAGGGATGATGAGA 221
QY 164 AAGGATCAGGAGAGAGGAGGAGATGCGAAGTGGGAGCATGGGGCGGAAGGAA 223
DB 222 CTGGATACGGGGGTCTTTGGGAAAGCTGGGAAAGATGGACCCAAAGGGGAGAGGCA 281
QY 224 TTAAGGAGAACTGGGTGATATGGAGATCGGGGCAATATTGGCAAGACTGGGCCATTG 283
DB 282 ATAAAGGATATAGGGGATTCGCGACCTGGGCTGATAGTAAATTTGGCCCAATTG 341
QY 284 GGAAGAGGTGACAAAGGGGAAAAGTTTCTTGGAAATCTCTGGAGAAAAGGCAAG 343
DB 342 GCAGCAAGAGGATTAAGGACATAAAGGCTTCCCGGCTTCCAGGAGGAAAGGAAAT 401
QY 344 CAGGTACTGTCTGTGATCTGGAAGATACCGGAAATTTTGGCAACTGATATTAGTA 403
DB 402 CAGGCACTTCTGTGATCTGGAAGATCCGCAAGTTGTGGCGAGCTGGAACCTTAATG 461
QY 404 TTGCCCGGTCAAGACATCTATGAATTTGTCAAGATGTGATACGAGGATTAGGAAA 463
DB 462 TTGGCAGCCTAAAGTCTTCCCTTAAATTTGTAAAAATGTGATTGCCGCGCATCAGGAAA 521

QY 464 CTGAGAGAAATTTACTACATCTGTCAGGAGAGAACTACAGGAATCCCTACCC 523
DB 522 CAGATGAGAGTACTATTATTCATTTGTGAGAGAGAGCGAACTACAGGATCGCTGACC 581
QY 524 ACTGAGGATTCGGGGTGAATGTCATGCCATGCCCAAGGATGAAGCTGCCAACAACATCA 583
DB 582 AGTGTCCGATAAGAGGGGTACTATTGGCAATGCCCAAGGATCAAGCTACCAATTCCTCA 641
QY 584 TCGCTGACTATGTTGCCAAGAGTGGCTTCTTCGGGTTCATTTGGCGTGAATGACCTTG 643
DB 642 TTGCTGATTCATCTCCAAATGCGGCTTTTCAGAGTATTTATAGGAATTAATGACATTG 701
QY 644 AAAGGGAGGAGACAGTACATGTTTCAGACACACACTCCCACTGCAGAACTATAGCACTGGA 703
DB 702 AGAAGAGAGAGCAGTTTGTGTATGATGATGATGATGATGATGATGATGATGATGATG 761
QY 704 ATGAGGGGAGACCCAGGACCCCTATGTCATGAGGACTGTGTGAGATGCTGAGCTCTG 763
DB 762 AAGCCGAGAGACCCAAACGATGGCTCTGGGTACGAACTGCTGGAATGCTCAGCACCG 821
QY 764 CAGATGGAATGACACAGAGTGCCATCTTACCATGTACTTTGTCTGTGAGTTTCATCAAGA 823
DB 822 GCCATTGACAGAGCTGGAGTCTGACCATCTACTTTGTCTGTGAGTTTCTGAAA 881
QY 824 AGAAGAAAG 831
DB 882 AGACAAG 889

RESULT 12
LOCUS CB228545
DEFINITION AGENCOURT_11505973 NICHD_Rh_Ov1 Macaca mulatta cDNA clone
IMAGE:6886251 5', mRNA sequence.
ACCESSION CB228545
VERSION CB228545
KEYWORDS EST.
SOURCE Macaca mulatta (rhesus monkey)
ORGANISM Macaca mulatta

REFERENCE 1 (bases 1 to 747)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Eliot Spindel
cDNA Library Preparation: CLONTECH
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLCW3139 row: a column: 02
High quality sequence stop: 526.

FEATURES
source
1. 747
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/mol_type="mRNA"
/db_xref="taxon:9544"
/clone="IMAGE:6886251"
/tissue_type="Ovary"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NICHD Rh_Ov1"
/note="Organ: ovary; Vector: pDNR-LIB; Site 1: Sfi I;
Site 2: Sfi I; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.0-4.0 kb. Tissue pooled from
pre-pubertal, post pubertal sn menopausal monkeys.
Constructed by Clontech. Note: this is a NICHD Library."

genome (LREG), Domaine de Vilvert, 78352, Jouy-en-Josas cedex, FRANCE, +33 (0) 1.34.55.28.02, +33 (0) 1.34.65.22.73
Sequence cleaned of vector, adaptor and repetitions. Contact us at sigenasupport@jouy.inra.fr to obtain the chromatogram of this sequence.

Plate: 0032 row: c column: 3.

FEATURES

source

Location/Qualifiers
1. .636
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="scac00321.c.03"
/tissue_type="mixed"

/clone_lib="Sus Scrofa library (scac)"
/notes="Vector: pT73D-pac vector; tissues: adipose tissue, brain, kidney, liver, muscle, ovary, testis, heart, hypothalamus, pancreas, skin, spleen, thymus, placenta, pituitary gland, seminal vesicle, small intestine, uterus, adrenal, bulbo urethral gland, cerebral trunk, epididymis, female gonad, gall-bladder, hippocampus, large intestine, male gonad, melanocytes, stomach, udder"

ORIGIN

Query Match 37.1%; Score 308.4; DB 13; Length 636;
Best Local Similarity 89.0%; Pred. No. 4.9e-74;
Matches 333; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Qy 458 GGGAACTGAAGAGAAATTTCTACTACATCGTCAGGAAGAGAACTACAGGGAATCCC 517
Db 1 GGGAAACGAGAGAAATTTCTACTACATCGTCAGGAGAGAGAACTACAGGGAATCCC 60

Qy 518 TAACCCACTGACGATTCGGGGTGGAAATGCTAGCCATGCCAAGGATGAAGTCCCAACA 577
Db 61 TGACCCACTCCGGATCCGGGGGGGATGTAGCCATGCCAAGGACGAAGTCCCAACA 120

Qy 578 CACTCATCGTGAATGTTGCCAAGAGTGGCTTTTCGGGTGTTTCATTCGGCTGATG 637
Db 121 CGTCTCTCGTGACTAGTCTCAGAGCGGCTTTTCGGGTGTTTCATTCGGGTGATG 180

Qy 638 ACCTTGAAAGGAGGACAGTACATGTTCCACAGACAACTCCACTGCAGAACTATAGCA 697
Db 181 ACCTGGAGAGGAGGAGGACAGTACGTTTCCACAGACAACTCCACTGCAGAACTATAGCA 240

Qy 698 ACTGGAGTGGGGAGACCAAGCCAGCCCTATGTCATGAGGACTGTGTGAGTGTGA 757
Db 241 ACTGGCAGGAGGAGTGGAGCCAGCCCTACGGTCAAGAGGACTGTGTGAAATGCTGA 300

Qy 758 GCTCTGCAGATGGAATGACACAGAGTGCATCTTACCATGTACTTTCTGTGAGTTCA 817
Db 301 GCTCGGCGAGATGGAATGACACAGGAGTGCCACTGACCATGTACTTTCTGTGAGTTG 360

Qy 818 TCAAGAGAAAAG 831
Db 361 TCAAGAGAAAAG 374

RESULT 15

BI067078

LOCUS

DEFINITION

pgfn.pk010.i8 normalized chicken fat cDNA library Gallus gallus
cDNA clone pgfn.pk010.i8 5' similar to gi|5453619 ref|NP_006429.1|
[Homo sapiens] dbj|BA01747.1| (C-type lectin); collectin liver 1
[Homo sapiens] dbj|BA01747.1| (AB002631) collectin 34 [Homo sapiens]G, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Gallus gallus (chicken)
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 654)

REFERENCE

AUTHORS
Cogburn, L.A., Morgan, R.W. and Burnside, J.
TITLE
Chicken ESTs from fat
JOURNAL
Unpublished (2001)
COMMENT
Contact: Larry A. Cogburn
University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1335
Fax: 302-831-2822
Email: cogburn@udel.edu, www.chickest.udel.edu.

FEATURES

source

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; Patent No. US20020169284A1
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; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
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; APPLICANT: Kuo, Sophia S.
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; APPLICANT: Pan, James;
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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
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 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
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 ; APPLICANT: Gerritsen, Mary E.
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 ; APPLICANT: Wood, William I.
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; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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;; PRIOR FILING DATE: 1998-04-22
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;; PRIOR APPLICATION NUMBER: 60/082796
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;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.08; Score 228; DB 9; Length 277;
Best Local Similarity 100.08; Pred. No. 6.9e-25;

Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNGFASLLRRNQFILLVFLVLLQSLGLDIDSRPTAEVCATHTISP 46
DB 1 MNGFASLLRRNQFILLVFLVLLQSLGLDIDSRPTAEVCATHTISP 46

RESULT 5

US-09-978-189-97
; Sequence 97, Application US/09978189
; Publication No. US20030004102A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C7
; CURRENT APPLICATION NUMBER: US/09/978,189
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
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;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 228; DB 10; Length 277;
Best Local Similarity 100.0%; Pred. No. 6.9e-25;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNGFASLLRRNQFILLVFLFIQISGLDIDSRPTAEVCATHISP 46
DB 1 MNGFASLLRRNQFILLVFLFIQISGLDIDSRPTAEVCATHISP 46

RESULT 6

US-09-978-608A-97
; Sequence 97, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gottard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C22

; CURRENT APPLICATION NUMBER: US/09/978, 608A
; NUMBER OF SEQ ID NOS: 624

; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 97
; LENGTH: 277

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-608A-97

Query Match 100.0%; Score 228; DB 10; Length 277;
Best Local Similarity 100.0%; Pred. No. 6.9e-25;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNGFASLLRRNQFILLVFLFIQISGLGIDSRPTAEVCATHHTISP 46
Db 1 MNGFASLLRRNQFILLVFLFIQISGLGIDSRPTAEVCATHHTISP 46

RESULT 7

US-09-978-585A-97
; Sequence 97, Application US/09978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gottard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C15

; CURRENT APPLICATION NUMBER: US/09/978, 585A

; NUMBER OF SEQ ID NOS: 624

; Prior Application removed - See File Wrapper or Palm

; SEQ ID NO 97

; LENGTH: 277

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-585A-97

Query Match 100.0%; Score 228; DB 10; Length 277;
Best Local Similarity 100.0%; Pred. No. 6.9e-25;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNGFASLLRRNQFILLVFLFIQISGLGIDSRPTAEVCATHHTISP 46
Db 1 MNGFASLLRRNQFILLVFLFIQISGLGIDSRPTAEVCATHHTISP 46

RESULT 8

US-09-978-191A-97
; Sequence 97, Application US/09978191A
; Publication No. US20030050239A1
; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gottard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C4

; CURRENT APPLICATION NUMBER: US/09/978, 191A

; Prior Application removed - See File Wrapper or Palm

; SEQ ID NO 97

; LENGTH: 277

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-191A-97

Query Match 100.0%; Score 228; DB 10; Length 277;
Best Local Similarity 100.0%; Pred. No. 6.9e-25;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNGFASLLRRNQFILLVFLFIQISGLGIDSRPTAEVCATHHTISP 46
Db 1 MNGFASLLRRNQFILLVFLFIQISGLGIDSRPTAEVCATHHTISP 46

PRIOR APPLICATION NUMBER: 60/081229	PRIOR FILING DATE: 1998-04-09
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PRIOR APPLICATION NUMBER: 60/084627	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084643	PRIOR FILING DATE: 1998-05-07
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; PRIOR FILING DATE: 1998-05-13
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; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 228; DB 10; Length 277;
Best Local Similarity 100.0%; Pred. No. 6.9e-25;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNGFASLLRRNQFILLVFLLIQSLGLDIDSRPTAEVCATHITSP 46
Db 1 MNGFASLLRRNQFILLVFLLIQSLGLDIDSRPTAEVCATHITSP 46

RESULT 9
US-09-978-403A-97
; Sequence 97, Application US/09978403A
; Publication No. US20030050240A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gottard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCES: P2630P1C17
; CURRENT APPLICATION NUMBER: US/09/978,403A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 09/918585
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; PRIOR APPLICATION NUMBER: 60/062250
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/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085704
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 228; DB 10; Length 277;
Best Local Similarity 100.0%; Pred. No. 6,9e-25; Indels 0; Caps 0;
Matches 46; Conservative 0; Mismatches 0;

QY 1 MNGFASLRRNQIFILLVFLLIQISGLDIDSRPTAEVCATHTISP 46
DB 1 MNGFASLRRNQIFILLVFLLIQISGLDIDSRPTAEVCATHTISP 46

RESULT 10

US-09-978-564A-97
/ Sequence 97, Application US/09978564A
/ Publication No. US20030050241A1
/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Botstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Eaton, Dan
/ APPLICANT: Ferrara, Napoleon
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth J.
/ APPLICANT: Kljavin, Ivar J.
/ APPLICANT: Kuo, Sophia S.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Shelton, David L.
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ TITLE OF INVENTION: Acids Encoding the Same
/ FILE REFERENCE: P2630P1C25
/ CURRENT APPLICATION NUMBER: US/09/978,564A
/ CURRENT FILING DATE: 2001-10-16
/ PRIOR APPLICATION NUMBER: 09/918585
/ PRIOR FILING DATE: 2001-07-30
/ PRIOR APPLICATION NUMBER: 60/062250
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/ PRIOR APPLICATION NUMBER: 60/077450
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Query Match 100.08; Score 228; DB 10; Length 277;
Best Local Similarity 100.08; Pred. No. 6.9e-25;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNGFASLLRRNQFILLVFLFIQISLGLDIDSRPTAEVCATHITSP 46
DB 1 MNGFASLLRRNQFILLVFLFIQISLGLDIDSRPTAEVCATHITSP 46

RESULT 11
US-09-999-833A-97
; Sequence 97, Application US/09999833A
; Publication No. US20030054405A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gottstein, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Pao, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC65
; CURRENT APPLICATION NUMBER: US/09/999,833A
; CURRENT FILING DATE: 2001-10-24
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Query Match	100.0%;	Score 228;	DB 10;	Length 277;
Best Local Similarity	100.0%;	Pred. No. 6.9e-25;		

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Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0
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Db 1 MNGFASLRNQFILLVFLFLLQISLGLDIDSRPTAEVCATHTISP 46

RESULT 12
US-09-981-915A-97
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; Publication No. US20030054986A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
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; APPLICANT: Kljavin, Ivar J.
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; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
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; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C12
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 / PRIOR FILING DATE: 1998-05-07
 / PRIOR APPLICATION NUMBER: 60/085339
 / PRIOR FILING DATE: 1998-05-13
 / PRIOR APPLICATION NUMBER: 60/085338
 / PRIOR FILING DATE: 1998-05-13
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 / PRIOR APPLICATION NUMBER: 60/085580
 / PRIOR FILING DATE: 1998-05-15
 / PRIOR APPLICATION NUMBER: 60/085573
 / PRIOR FILING DATE: 1998-05-15
 / PRIOR APPLICATION NUMBER: 60/085704
 / PRIOR FILING DATE: 1998-05-15
 / PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 228; DB 10; Length 277;

Best Local Similarity 100.0%; Pred. No. 6.9e-25; Matches 46; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 MNGFASLRNRQFILLVLFLIQSLGLDIDSRPTAEVCATHTISP 46

DB 1 MNGFASLRNRQFILLVLFLIQSLGLDIDSRPTAEVCATHTISP 46

RESULT 13

US-09-978-824-97
; Sequence 97, Application US/09978824
; Publication No. US20030055216A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P.C14
; CURRENT APPLICATION NUMBER: US/09/978,824
; CURRENT FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
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; PRIOR FILING DATE: 1998-03-27
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; PRIOR FILING DATE: 1998-03-27
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; PRIOR FILING DATE: 1998-04-28
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; PRIOR FILING DATE: 1998-04-29
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; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083496

APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C1
CURRENT APPLICATION NUMBER: US/09/918,585A
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
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PRIOR APPLICATION NUMBER: 60/065311
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PRIOR APPLICATION NUMBER: 60/066364
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PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079920

Query Match 100.0%; Score 228; DB 10; Length 277;
Best Local Similarity 100.0%; Pred. No. 6,9e-25;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 MNGPASILRRNQIFLLVFLFQIQSLGLDIDSRPTAEVCATHTISP 46
Db 1 MNGPASILRRNQIFLLVFLFQIQSLGLDIDSRPTAEVCATHTISP 46

RESULT 14

US-09-918-585A-97
Sequence 97, Application US/09918585A
Publication No. US2003060406A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.

;; PRIOR FILING DATE: 1998-03-30
;; PRIOR APPLICATION NUMBER: 60/079923
;; PRIOR FILING DATE: 1998-03-30
;; PRIOR APPLICATION NUMBER: 60/080105
;; PRIOR FILING DATE: 1998-03-31
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Query Match 100.0%; Score 228; DB 10; Length 277;
Best Local Similarity 100.0%; Pred. No. 6.9e-25;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNGFASLLRRNQFILLVLFLQIQSLGLDIDSDRPTAEVCATHTISP 46

Db 1 MNGFASLLRRNQFILLVLFLQIQSLGLDIDSDRPTAEVCATHTISP 46

RESULT 15

US-09-978-423A-97
; Sequence 97, Application US/09978423A
; Publication No. US2003069178A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC21
CURRENT APPLICATION NUMBER: US/09/978,423A
CURRENT FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
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PRIOR FILING DATE: 1998-03-12
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1 PRIOR FILING DATE: 1998-04-30
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1 PRIOR FILING DATE: 1998-05-15
1 PRIOR APPLICATION NUMBER: 60/085573
1 PRIOR FILING DATE: 1998-05-15
1 PRIOR APPLICATION NUMBER: 60/085704
1 PRIOR FILING DATE: 1998-05-15
1 PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 228; DB 10; Length 277;
Best Local Similarity 100.0%; Pred. No. 6.9e-25;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 MNGFASLRRNQFILLVLFLLIQSLGLDIDSRPTAEVCATHTISP 46
Db 1 MNGFASLRRNQFILLVLFLLIQSLGLDIDSRPTAEVCATHTISP 46

Search completed: March 8, 2004, 12:18:56
Job time : 17.6167 secs

GenCore version 5.1.6
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DM protein - protein search, using sw model

Run on: March 8, 2004, 11:56:05 ; Search time 7.29515 Seconds
(without alignments)

328.331 Million cell updates/sec

Title: US-09-600-932-2_COPY_1_46

Perfect score: 228

Sequence: 1 MNGFASLLRNQFILLVLF.....GLDIDSRPTAEVCATHHTISP 46

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

result	No.	Score	Query Match	Length	DB ID	Description
1	55	24.1	313	1	OAKL_HUMAN	Q89X5 homo sapien
2	52	22.8	130	1	OAXE_MOUSE	O55241 mus musculus
3	52	22.8	130	1	OAXE_RAT	O55232 rattus norv
4	51	22.4	77	1	SECQ_MYCGE	P58061 mycoplasma
5	51	22.4	1077	1	B2K3_CABEL	Q19192 caenorhabdi
6	50.5	22.1	331	1	RBSR_HAEIN	P44329 haemophilus
7	50.5	22.1	372	1	S17B_HUMAN	O94768 homo sapien
8	50	21.9	168	1	X027_MYCFN	P75084 mycoplasma
9	50	21.9	281	1	CD37_RAT	P31053 rattus norv
10	50	21.9	817	1	FTSK_BRUME	O8YJ58 bruceella me
11	50	21.9	854	1	FTSK_BRUSU	O8FY10 bruceella su
12	49.5	21.7	182	1	YLH9_CABEL	P34363 caenorhabdi
13	49	21.5	105	1	P679_TREPA	O83685 treponema p
14	49	21.5	484	1	PER2_VOLCA	P81132 volvox cart
15	48.5	21.3	228	1	COX2_AEDAE	P50892 aedes aegypt
16	48.5	21.3	228	1	COX2_CULQU	P50893 culex quinq
17	48.5	21.3	747	1	Y030_UREPA	O9PRB5 ureaplasma
18	48	21.1	259	1	UPKB_MUSVI	P30413 mustela vis
19	48	21.1	1118	1	PHY_ADICA	P42496 adiantum ca
20	47.5	20.8	134	1	ATPE_CHLVU	P32979 chlorella v
21	47.5	20.8	318	1	BST1_HUMAN	Q10588 homo sapien
22	47.5	20.8	349	1	OPSG_CARAU	P32311 caecilius a
23	47.5	20.8	360	1	WNT2_CABEL	P34889 caenorhabdi
24	47.5	20.8	715	1	NSR1_PSAEA	O9HY13 pseudomonas
25	47.5	20.8	807	1	YB9T_YEAST	P38148 saccharomyc
26	47.5	20.8	2703	1	NOTC_DROME	P07207 drosophila
27	47	20.6	76	1	SECQ_MYCFN	O9EXD0 mycoplasma
28	47	20.6	166	1	YA43_HAEIN	P44101 haemophilus
29	47	20.6	214	1	YENI_YEREN	P52388 yersinia en
30	47	20.6	282	1	AURC_MOUSE	O88445 mus musculu
31	47	20.6	309	1	AURC_HUMAN	O9U659 homo sapien
32	47	20.6	319	1	BST1_RAT	Q63072 rattus norv
33	47	20.6	376	1	CPR2_ARATH	O91XW3 arabidopsis

RESULT 1

ID	OAKL_HUMAN	STANDARD;	PRT;	313 AA.
AC	Q89X5;			
DT	10-OCT-2003 (Rel. 42, Created)			
DT	10-OCT-2003 (Rel. 42, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Olfactory receptor 10K1.			
GN	OR10K1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,			
RA	Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;			
RT	"Genome-wide discovery and analysis of human seven transmembrane helix			
RT	receptor genes.";			
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.			
CC	-!- FUNCTION: Putative odorant receptor.			
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.			
CC	-!- DATABASE: NAME=Human Olfactory Receptor Data Exploratorium (HORDE);			
CC	WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbols			
CC	-----			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
CC	EMBL; AB065641; BAC05867.1; --			
DR	Genew; HGNC:14693; OR10K1.			
DR	InterPro; IPR000276; GPCR_Rhodpsn.			
DR	Pfam; PF00001; 7tm_1; 1.			
DR	PRINTS; PR00237; GPCRHOPOSPN.			
DR	PROSITE; PS00237; G-PROTEIN RECEPT_F1.1; FALSE_NEG.			
DR	PROSITE; PS00262; G-PROTEIN RECEPT_F1.2; 1.			
KW	G-protein coupled receptor; Transmembrane; Glycoprotein;			
KW	Multigene family; Olfaction.			
FT	DOMAIN 1 25			
FT	TRANSMEM 26 46			
FT	DOMAIN 47 54			
FT	TRANSMEM 55 75			
FT	DOMAIN 76 99			
FT	TRANSMEM 100 120			
FT	DOMAIN 121 139			
FT	TRANSMEM 140 160			
FT	DOMAIN 161 197			
FT	TRANSMEM 198 217			
FT	DOMAIN 218 237			
FT	TRANSMEM 238 258			
FT	DOMAIN 259 271			
FT	EXTRACELLULAR (POTENTIAL).			
FT	1 (POTENTIAL).			
FT	2 (POTENTIAL).			
FT	3 (POTENTIAL).			
FT	4 (POTENTIAL).			
FT	5 (POTENTIAL).			
FT	6 (POTENTIAL).			
FT	EXTRACELLULAR (POTENTIAL).			

FT TRANSMEM 272 292 7 (POTENTIAL).
FT DOMAIN 293 313 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 5 5 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 265 265 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 313 AA; 35079 MW; 96E546B9EC492965 CRC64;
Query Match 24.1%; Score 55; DB 1; Length 313;
Best Local Similarity 25.0%; Pred. No. 3.5;
Matches 16; Conservative 9; Mismatches 19; Indels 20; Gaps 1;
2Y 3 GFASLLRRNPFLLVLLFLLQISGLDIDSRPT-----AEVCATH 42
2b 16 GFSSLRQLQLFVFLFLLVFLFLLTNAIISIVLDRLHFWFFLLSCSHICVTF 75
2Y 43 TISP 46
2b 76 VIVP 79
RESULT 2
DREX_MOUSE STANDARD; PRT; 130 AA.
AC O55241;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Orexin precursor (Hypocretin) (Hcrt) [Contains: Orexin-A (Hypocretin-1) (Hcrt1); Orexin-B (Hypocretin-2) (Hcrt2)].
Hcrt OR OX OR PPOX.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A., PubMed=9491897;
MEDLINE=98150861;
Sakurai T., Amemiya A., Ishii M., Matsuzaki I., Chenelli R.M., Tanaka H., Williams S.C., Richardson J.A., Kozlowski G.P., Wilson S., Arch J.R.S., Buckingham R.E., Haynes A.C., Carr S.A., Annan R.S., McNulty D.E., Liu W.-S., Terrett J.A., Elshourbagy N.A., Bergsma D.J., Yanagisawa M., Yanagisawa M.;
"Orexins and orexin receptors: a family of hypothalamic neuropeptides and G protein-coupled receptors that regulate feeding behavior."; Cell 92:573-585(1998).
[2]
SEQUENCE FROM N.A.
STRAIN=CS7BL/6J;
RC MEDLINE=98081872; PubMed=9419374;
de Lecea L., Kilduff T.S., Peyron C., Gao X.-B., Foye P.E., Danielson P.E., Fukuhara C., Battenberg E.L.F., Gautvik V.T., Bartlett P.S. II, Frankel W.N., van den Pol A.N., Bloom F.E., Gautvik K.M., Sutcliffe J.G.;
"The hypocretins: hypothalamus-specific peptides with neuroexcitatory activity."; Proc. Natl. Acad. Sci. U.S.A. 95:322-327(1998).
[3]
REVIEW
RX MEDLINE=21237974; PubMed=11340621;
Hungs M., Mignot E.;
"Hypocretin/orexin, sleep and narcolepsy."; Bioessays 23:397-408(2001).
[4]
REVIEW
RX MEDLINE=21178476; PubMed=11283317;
Willie J.T., Chenelli R.M., Sinton C.M., Yanagisawa M.;
"To eat or to sleep? Orexin in the regulation of feeding and wakefulness.";
RX ANNU. REV. NEUROSCI. 24:429-458(2001).
-!- FUNCTION: Neuropeptides that play a significant role in the regulation of food intake and sleep-wakefulness, possibly by coordinating the complex behavioral and physiologic responses of these complementary homeostatic functions. A broader role in the homeostatic regulation of energy metabolism, autonomic function,

CC hormonal balance and the regulation of body fluids, is also suggested. Orexin-A binds to both OX1R and OX2R with a high affinity, whereas orexin-B binds only to OX2R with a similar affinity.
CC -!- SUBCELLULAR LOCATION: ASSOCIATED WITH PERIKARYAL ROUGH ENDOPLASMIC RETICULUM AS WELL AS CYTOPLASMIC LARGE GRANULAR VESICLES AT SYNAPSES (BY SIMILARITY).
CC -!- TISSUE SPECIFICITY: RESTRICTED TO NEURONAL CELL BODIES OF THE DORSAL AND LATERAL HYPOTHALAMUS.
CC -!- PTM: Specific enzymatic cleavages at paired basic residues yield the different active peptides.
CC -!- SIMILARITY: Belongs to the orexin family.
CC -!- DATABASE: NAME-Protein Spotlight;
CC NOTE-Issue 15 of October 2001,
CC WWW="http://www.expasy.org/spotlight/articles/splt015.html".
CC -----
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CC -----
CC EMBL; AF041242; AAC40040.1; -;
CC EMBL; AF019566; AAC02934.1; -;
CC MGD; MGI:1202306; Hcrt.
CC InterPro; IPR001704; Orexin.
CC Pfam; PF02072; Orexin; 1
CC PRINTS; PR01091; OREXINPP.
CC Neuropeptide; Cleavage on pair of basic residues; Signal; Amidation;
KW Pyroglutamate carboxylic acid.
FT SIGNAL 1 32 BY SIMILARITY.
FT PEPTIDE 33 65 OREXIN-A.
FT PROPEP 97 130 OREXIN-B.
FT MOD_RES 33 33 PYRROLIDONE CARBOXYLIC ACID (BY SIMILARITY).
FT MOD_RES 65 65 SIMILARITY.
FT MOD_RES 96 96 AMIDATION (G-66 PROVIDE AMIDE GROUP) (BY SIMILARITY).
FT DISULFID 38 44 BY SIMILARITY.
FT DISULFID 39 46 BY SIMILARITY.
SQ SEQUENCE 130 AA; 13503 MW; D3C223F9EB835F1C CRC64;
Query Match 22.8%; Score 52; DB 1; Length 130;
Best Local Similarity 38.7%; Pred. No. 3.8;
Matches 12; Conservative 5; Mismatches 14; Indels 0; Gaps 0;
Qy 15 LVLFLQLQISGLDIDSRPTAEVCATHFIS 45
Db 15 LLLLLLPPALLSLGVDAQPLPDCRCQKTC 45
RESULT 3
DREX_MOUSE STANDARD; PRT; 130 AA.
AC O55232;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Orexin precursor (Hypocretin) (Hcrt) [Contains: Orexin-A (Hypocretin-1) (Hcrt1); Orexin-B (Hypocretin-2) (Hcrt2)].
Hcrt OR OX OR PPOX.
Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
[1]
SEQUENCE FROM N.A., AND SEQUENCE OF 33-65 AND 69-96.
RC TISSUE=Brain;
RX MEDLINE=98150861; PubMed=9491897;

RA Sakurai T., Amemiya A., Ichii M., Matsuzaki I., Chemelli R.M.,
RA Tanaka H., Williams S.C., Richardson J.A., Kozlowski G.P., Wilson S.,
RA Arch J.R.S., Buckingham R.E., Haynes A.C., Carr S.A., Annan R.S.,
RA McNulty D.E., Liu W.-S., Terrett J.A., Elshourbagy N.A., Bergsma D.J.,
RA Yanagisawa M.;
RT "Orexins and orexin receptors: a family of hypothalamic neuropeptides
RT and G protein-coupled receptors that regulate feeding behavior.";
RL Cell 92:573-585(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=Sprague-Dawley;
RX MEDLINE=98081872; PubMed=9419374;
RA De Lecea L., Kilduff T.S., Peyron C., Gao X.-B., Foye P.E.,
RA Danielson P.E., Fukuhara C., Battenberg E.L.F., Gautvik V.T.,
RA Bartlett F.S. II, Frankel W.N., van den Pol A.N., Bloom F.E.,
RA Gautvik K.M., Sutcliffe J.G.;
RT "The hypocretins: hypothalamus-specific peptides with neuroexcitatory
RT activity.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:322-327(1998).
RN [3]
RP REVIEW.
RX Hungs M., Mignot E.;
RX MEDLINE=21237974; PubMed=11340621;
RA "Hypocretin/orexin, sleep and narcolepsy.";
RL Bioessays 23:397-408(2001).
RN [4]
RP REVIEW.
RX MEDLINE=21178476; PubMed=11283317;
RA Willie J.T., Chemelli R.M., Sinton C.M., Yanagisawa M.;
RA "To eat or to sleep? Orexin in the regulation of feeding and
RA wakefulness.";
RL Annu. Rev. Neurosci. 24:429-458(2001).
CC -|- FUNCTION: Neuropeptides that play a significant role in the
CC regulation of food intake and sleep-wakefulness, possibly by
CC coordinating the complex behavioral and physiologic responses of
CC these complementary homeostatic functions. A broader role in the
CC homeostatic regulation of energy metabolism, autonomic function,
CC hormonal balance and the regulation of body fluids, is also
CC suggested. A modulation effect on luteinizing hormone-releasing
CC hormone (LHRH) secretion also suggests a more minor contribution
CC to the regulation of reproductive function. Orexin-A binds to both
CC OX1R and OX2R with a high affinity, whereas orexin-B binds only to
CC OX2R with a similar high affinity.
CC -|- SUBCELLULAR LOCATION: ASSOCIATED WITH PERIKARYAL ROUGH ENDOPLASMIC
CC RETICULUM AS WELL AS CYTOSOLIC LARGE GRANULAR VESICLES AT
CC SYNAPSES.
CC -|- TISSUE SPECIFICITY: Produced by a small group of neurons
CC restricted to the lateral and posterior hypothalamus and
CC perifornical areas. Positive neurons project widely throughout the
CC entire neuroaxis. Particularly abundant projections in the
CC cerebral cortex, olfactory bulb, hippocampus, amygdala, septum,
CC diagonal band of Broca, bed nucleus of the stria terminalis,
CC thalamus, anterior and posterior hypothalamus, midbrain,
CC brainstem, and spinal cord. Immunoreactivity reported in the
CC enteric nervous system and pancreas. In small amount, also
CC detected in the testis.
CC -|- DEVELOPMENTAL STAGE: DETECTED AS EARLY AS EMBRYONIC DAY 18, BUT
CC EXPRESSION INCREASED DRAMATICALLY AFTER THE THIRD POSTNATAL WEEK.
CC -|- INDUCTION: By nutritional state, up-regulated by fasting, fluid
CC deprivation and insulin-induced hypoglycemia. Orexin-A
CC immunoreactivity varies diurnally and peaks during the dark
CC phase, in the pons and the location of locus coeruleus.
CC -|- PTM: Specific enzymatic cleavages at paired basic residues yield
CC the different active peptides.
CC -|- MASS SPECTROMETRY: MW=3558.7; MW_ERR=0.1; METHOD=MALDI;
CC RANGES=33-65.
CC -|- SIMILARITY: Belongs to the orexin family.
CC -|- DATABASE: NAME-Protein Spotlight;
CC NOTE=Issue 15 of October 2001;
CC WWW="http://www.expasy.org/spotlight/articles/spot015.html".
CC -----
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CC -----
CC EMBL: AF041241; AAC40039.1; -;
CC EMBL: AF019565; AAC02933.1; -;
CC InterPro: IPR001704; Orexin.
CC Pfam: PF02072; Orexin; 1.
CC PRINTS: PR01091; OREXINPP.
CC KW Neuropeptide; Cleavage on pair of basic residues; Signal; Amidation;
CC FT PYROLIDONE CARBOXYLIC ACID.
CC SIGNAL 1 32
CC PEPTIDE 33 65 OREXIN-A.
CC PEPTIDE 69 96 OREXIN-B.
CC PROPEP 97 130
CC FT MOD RES 33 33 PYRROLIDONE CARBOXYLIC ACID.
CC FT MOD RES 65 65 AMIDATION (G-66 PROVIDE AMIDE GROUP).
CC FT MOD RES 96 96 AMIDATION (G-97 PROVIDE AMIDE GROUP).
CC FT DISULFID 38 44
CC FT DISULFID 39 45
CC SQ SEQUENCE 130 AA; 13645 MW; 00CAB259EDF2A404 CRC64;
CC Query Match 22.8%; Score 52; DB 1; Length 130;
CC Best Local Similarity 38.7%; Pred. No. 3.8;
CC Matches 12; Conservative 5; Mismatches 14; Indels 0; Gaps 0;
QY 15 LVLVFLQLQISGLDIDSRPTAEVCATHIS 45
DB 15 LLLLLLPPALLSLGVDAQPLDCCRQKTC 45
RESULT 4
SECG MYCGE STANDARD; PRT; 77 AA.
AC PS8081; 2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable protein-export membrane protein secg.
GN SECG OR MG103.1.
OS Mycoplasma genitalium.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2097;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 33530 / G-37;
RX MEDLINE=96026346; PubMed=7569993;
RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhmann J.D.,
RA Nguyen D.T., Uterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
RA Tomb J.-P., Dougherty B.A., Bitt K.F., Hu P.-C., Lucier T.S.,
RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RT "The minimal gene complement of Mycoplasma genitalium.";
RL Science 270:397-403(1995).
RN [2]
RP IDENTIFICATION.
RX Medigue C., Bocs S.;
RL Unpublished observations (MAY-2001).
CC -|- FUNCTION: Involved in protein export. Participates in an early
CC event of protein translocation (By similarity).
CC -|- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -|- SIMILARITY: Belongs to the secg family.
CC -----
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CC EMBL; U39690; -; NOT_ANNOTATED_CDS.
DR EMBL; U39691; -; NOT_ANNOTATED_CDS.
DR TIGS; MG103.1; -.
KW Protein transport; Translocation, Transmembrane; Complete proteome.
FT TRANSMEM 3 23 POTENTIAL.
FT TRANSMEM 56 76 POTENTIAL.
SQ SEQUENCE 77 AA; 8543 MW; F4AA12D8EDBBS6D CRC64;
Query Match 22.4%; Score 51; DB 1; Length 77;
Best Local Similarity 43.8%; Pred. No. 3.1;
Matches 14; Conservative 4; Mismatches 10; Indels 4; Gaps 1;
2Y 3 GPASLLRRNQFILLVFLQISGLGIDSRP 34
3B 49 GFVKILQINFILVFLFI-----LGLIFSAP 76
RESULT 5
EZK3 CAEEL
ID E2K3 CAEEL STANDARD; PRT; 1077 AA.
AC Q19192; Q20459;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Eukaryotic translation initiation factor 2-alpha kinase precursor
DE (EC 2.7.1.1-) (PRK-like endoplasmic reticulum kinase) (PERK) (PERK) (CEPK).
DE (CEPK).
GN PEK-1 OR EIF2AK3 OR F46C3.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RX MEDLINE=20143423; PubMed=10677345;
RA Sood R., Porter A.C., Ma K., Quilliam L.A., Wek R.C.;
RT "Pancreatic eukaryotic initiation factor-2alpha kinase (PERK) homologues that mediate Drosophila melanogaster and Caenorhabditis elegans at human, Drosophila melanogaster and Caenorhabditis reticulum stress";
RT Biochem. J. 346:281-293 (2000).
RL [2]
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638094; PubMed=11779465;
RA Shen X., Ellis R.E., Lee K., Liu C.-Y., Yang K., Solomon A., Yoshida H., Morimoto R., Kunit D.M., Mori K., Kaufman R.J.;
RT "Complementary signaling pathways regulate the unfolded protein response and are required for C. elegans development.";
RL Cell 107:893-903 (2001).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=Bristol N2;
RA Dobson R., Cottage A.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Phosphorylates the alpha subunit of eukaryotic translation-initiation factor 2 (EIF2), leading to its inactivation and thus to a rapid reduction of translational initiation and repression of global protein synthesis.
CC -!- ENZYME REGULATION: Perturbation in protein folding in the endoplasmic reticulum (ER) promotes reversible dissociation from HSPA5/BIP and oligomerization, resulting in transautophosphorylation and kinase activity induction (By similarity).
CC -!- SUBUNIT: FORMS DIMERS WITH HSPA5/BIP IN RESTING CELLS (BY SIMILARITY). OLIGOMERIZES IN ER-STRESSED CELLS.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Endoplasmic reticulum (By similarity).
CC -!- INDUCTION: By ER stress.
CC -!- DOMAIN: The luminal domain senses perturbations in protein folding in the ER, probably through reversible interaction with HSPA5/BIP (By similarity).
CC -!- PTM: Autophosphorylated (By similarity).

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CC CC -!- PTM: N-glycosylated (By similarity).
CC CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. GCN2 subfamily.
CC CC
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CC CC
CC CC EMBL; AF193341; AAF61201.1; -.
CC CC EMBL; AF435953; AAL30829.1; -.
CC CC EMBL; Z68104; CAA92117.1; -.
CC CC EMBL; Z66563; CAA92117.1; JOINED.
CC CC EMBL; Z66563; CAA91470.1; -.
CC CC EMBL; Z68104; CAA91470.1; JOINED.
CC CC PIR; T20579; T20579.
CC CC WormPep; F46C3.1; CE18695.
CC CC InterPro; IPR000719; Prot_kinase.
CC CC InterPro; IPR008271; Ser_Thr_pkin_AS.
CC CC Pfam; PF00069; pkinase; 1.
CC CC ProDom; PD000001; Prot_kinase; 2.
CC CC SMART; SMO0564; PQ; 1.
CC CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC CC PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
CC CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC CC Serine/threonine-protein kinase; transferase; Translation regulation; unfolded protein response; Endoplasmic reticulum; Phosphorylation; ATP-binding; Signal; Transmembrane; Glycoprotein.
CC CC SIGNAL 1 23 POTENTIAL.
CC CC CHAIN 24 1077 EUKARYOTIC TRANSLATION INITIATION FACTOR 2-ALPHA KINASE.
CC CC DOMAIN 24 453 LUMENAL (POTENTIAL).
CC CC TRANSMEM 454 474 POTENTIAL.
CC CC DOMAIN 475 1077 CYTOPLASMIC (POTENTIAL).
CC CC DOMAIN 604 1076 PROTEIN_KINASE.
CC CC NP_BIND 610 618 ATP (BY SIMILARITY).
CC CC BINDING 633 633 ATP (BY SIMILARITY).
CC CC DOMAIN 794 808 SER-RICH.
CC CC ACT_SITE 933 933 BY SIMILARITY.
CC CC CARBOHYD 206 206 N-LINKED (GLCNAC...), (POTENTIAL).
CC CC SEQUENCE 1077 AA; 119638 MW; DA15615994FC36EC CRC64;
Query Match 22.4%; Score 51; DB 1; Length 1077;
Best Local Similarity 54.2%; Pred. No. 46;
Matches 13; Conservative 2; Mismatches 7; Indels 2; Gaps 1;
QY 19 FLIQISGLGIDSRPTAEVCATH 42
DB 1052 FLQIQTSL--LEPSRPTAEVATH 1073
RESULT 6
RBSR HABIN
ID RBSR HABIN STANDARD; PRT; 331 AA.
AC P44329;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Ribose operon repressor.
DE RBSR OR H10506.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D.; Adams M.D.; White O.; Clayton R.A.; Kirkness E.F.; Kerlavage A.R.; Bult C.J.; Tomb J.-F.; Dougherty B.A.; Merrick J.M.;

```


Matches 11; Conservative 6; Mismatches 4; Indels 1; Gaps 1;

QY 23 IQSLGL-DIDGRPAEVCATHT 43
||| : : : ||| : : :
Db 270 IQSLLVKPKPEKPAEICLSHS 291
||| : : : ||| : : :
RESULT 8
ID Y027 MYCPN STANDARD; PRT; 168 AA.
AC P75084;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MG027 homolog (B01_orf168).
GN MPN030 OR MP124.
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
CX NCBI_TaxID=2104;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 29342 / M129;
RX MEDLINE=97105885; PubMed=8948633;
RA Himmelreich R., Hilbert H., Plogers H., Pirkel E., Li B.-C.,
RA Herkmann R.;
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
RT pneumoniae";
RL Nucleic Acids Res. 24:4420-4449(1996).
CC -----
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CC -----
CC EMBL; AB000015; AAB95772.1; -;
DR PIR; S73450; S73450.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 168 AA; 19214 MW; C37192BBA3A82D4B CRC64;

Query Match 21.9%; Score 50; DB 1; Length 168;
Best Local Similarity 39.6%; Pred. No. 9.5;
Matches 19; Conservative 2; Mismatches 13; Indels 14; Gaps 3;

QY 1 MNGFASLLRRNQ-----FILLVFLLL-----IQSLGLDID--SRP 34
||| : : : ||| : : : ||| : : :
Db 22 VNGTTSKLTQRTQRTAIVEIFATLFLPKTADQIQAFLLDYDVP 69
||| : : : ||| : : : ||| : : :
RESULT 9
ID CD37 RAT STANDARD; PRT; 281 AA.
AC P31053;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Leukocyte antigen CD37.
GN CD37.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PVG X DA;
RX MEDLINE=90354767; PubMed=2388030;
RA Classon B.J., Williams A.F., Willis A.C., Seed B., Stamenkovic I.;
RT "The primary structure of the human leukocyte antigen CD37, a species
RT homologue of the rat MRC OX-44 antigen";
RJ. Exp. Med. 172:1007-1007(1990).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- TISSUE SPECIFICITY: B lymphocytes.
CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
CC -----
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CC -----
CC EMBL; X53517; CAA37596.1; -;
DR PIR; B47629; B47629.
DR InterPro; IPR000301; Transmem 4.
DR Pfam; PF00335; Transmembrane7; 1.
DR PRINTS; PR00259; TMFOUR.
DR PROSITE; PS00421; TM4_1; 1.
KW Glycoprotein; Antigen; Transmembrane.
CX NCBI_TaxID=2104;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=16M / ATCC 23456 / Biotype 1;
RX MEDLINE=20020109; PubMed=11756688;
RA DelVecchio V.G., Kapral V., Redkar R.J., Patra G., Mujar C., Los T.,
RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,
RA Jablonka L., Larsen N., D'Souza M., Bernal A., Mazur M., Goldsman E.,
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA Haselkorn R., Kyriades N., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis";
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
CC -!- FUNCTION: DNA motor protein, which is both required to move DNA
CC out of the region of the septum during cell division and for the
CC septum formation. Tracks DNA in an ATP-dependent manner by
CC generating positive supercoils in front of it and negative
CC supercoils behind it (By similarity).
CC -!- SUBUNIT: Homodimer. This suggests the formation of a ring
CC between the two cells at the septum that surrounds DNA (By

Query Match 21.9%; Score 50; DB 1; Length 281;
Best Local Similarity 47.8%; Pred. No. 16;
Matches 11; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 18 LFLQLQSLGLDIDSRPAEVC 40
||| : : : ||| : : : ||| : : :
Db 196 LFLQLSRLGLGFRALRQTADICA 218
||| : : : ||| : : : ||| : : :
RESULT 10
ID FTSK BRUME STANDARD; PRT; 817 AA.
AC Q8XJB8;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE DNA translocase ftsK.
GN FTSK OR BME10168.
OS Brucella melitensis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
CX NCBI_TaxID=29459;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=16M / ATCC 23456 / Biotype 1;
RX MEDLINE=20020109; PubMed=11756688;
RA DelVecchio V.G., Kapral V., Redkar R.J., Patra G., Mujar C., Los T.,
RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,
RA Jablonka L., Larsen N., D'Souza M., Bernal A., Mazur M., Goldsman E.,
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA Haselkorn R., Kyriades N., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis";
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
CC -!- FUNCTION: DNA motor protein, which is both required to move DNA
CC out of the region of the septum during cell division and for the
CC septum formation. Tracks DNA in an ATP-dependent manner by
CC generating positive supercoils in front of it and negative
CC supercoils behind it (By similarity).
CC -!- SUBUNIT: Homodimer. This suggests the formation of a ring
CC between the two cells at the septum that surrounds DNA (By

```
CC similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Located at the
CC septum. The large C-terminal part of the protein is cytoplasmic
CC (Potential).
CC -!- SIMILARITY: Contains 1 FtsK domain.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AC009459; AAL51350.1; ALT_INIT.
CC DR PIR; AC3273; AC3273.
CC DR HAMAP; MF_01809; -.
CC DR InterPro; IPR003593; AAA_ATPase.
CC DR Pfam; PF01580; FtsK_SpoIIIE.
CC DR SMART; SM00382; AAA; 1.
CC DR PROSITE; PS0501; FTSK; 1.
CC KW Chromosome partition; Cell division; ATP-binding; DNA-binding;
CC Transmembrane; Complete proteome.
CC FT TRANSMEM 31 53 POTENTIAL.
CC FT TRANSMEM 83 105 POTENTIAL.
CC FT TRANSMEM 118 140 POTENTIAL.
CC FT TRANSMEM 144 166 POTENTIAL.
CC FT TRANSMEM 173 195 POTENTIAL.
CC FT DOMAIN 452 671 FTSK.
CC FT NP_BIND 489 476 ATP (POTENTIAL).
CC SQ SEQUENCE 817 AA; 88805 MW; 7F94030ACAC316DF CRC64;
Query Match 21.9%; Score 50; DB 1; Length 817;
Best Local Similarity 44.0%; Pred. No. 48;
Matches 11; Conservative 7; Mismatches 7; Indels 0; Gaps 0;
QY 4 FASLRRNQFILLVFLFQIQSLGL 28
DB 23 FANLVRQVYILLGLGLSLTAMAV 47
RESULT 11
ID_FTSK_BRUSU STANDARD; PRT; 854 AA.
AC Q8FYI0;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE DNA translocase ftsK.
GN FTSK OR BR1895.
OS Brucella suis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29461;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1310 / Biovar 1;
RX MEDLINE=22247741; PubMed=12271122;
RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
RA Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,
RA Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
RA Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E.,
RA Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,
RA Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.;
RT "The Brucella suis genome reveals fundamental similarities between
RT animal and plant pathogens and symbionts."
RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
CC -!- FUNCTION: DNA motor protein, which is both required to move DNA
CC out of the region of the septum during cell division and for the
CC septum formation. Tracks DNA in an ATP-dependent manner by
CC generating positive supercoils in front of it and negative
CC supercoils behind it (By similarity).
```

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CC -!- SUBUNIT: Homohexamer. This suggests the formation of a ring
CC between the two cells at the septum that surrounds DNA (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Located at the
CC septum. The large C-terminal part of the protein is cytoplasmic
CC (Potential).
CC -!- SIMILARITY: Contains 1 FtsK domain.
CC
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CC
CC EMBL; AE014479; AAN30788.1; -.
CC DR TIGR; BR1895; -.
CC DR HAMAP; MF_01809; -.
CC DR InterPro; IPR003593; AAA_ATPase.
CC DR InterPro; IPR002543; FtsK_SpoIIIE.
CC DR Pfam; PF01580; FtsK_SpoIIIE; 1.
CC DR SMART; SM00382; AAA; 1.
CC DR PROSITE; PS0501; FTSK; 1.
CC KW Chromosome partition; Cell division; ATP-binding; DNA-binding;
CC Transmembrane; Complete proteome.
CC FT TRANSMEM 31 53 POTENTIAL.
CC FT TRANSMEM 83 105 POTENTIAL.
CC FT TRANSMEM 118 140 POTENTIAL.
CC FT TRANSMEM 144 166 POTENTIAL.
CC FT TRANSMEM 173 195 POTENTIAL.
CC FT DOMAIN 489 708 FTSK.
CC FT NP_BIND 506 513 ATP (POTENTIAL).
CC SQ SEQUENCE 854 AA; 92779 MW; 2BD08EP8B5454CAC CRC64;
Query Match 21.9%; Score 50; DB 1; Length 854;
Best Local Similarity 44.0%; Pred. No. 50;
Matches 11; Conservative 7; Mismatches 7; Indels 0; Gaps 0;
QY 4 FASLRRNQFILLVFLFQIQSLGL 28
DB 23 FANLVRQVYILLGLGLSLTAMAV 47
RESULT 12
ID_YLH9_CAEEL STANDARD; PRT; 182 AA.
AC P34363;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein C48B4.9 in chromosome III.
GN C48B4.9.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Copsey T., Cooper J., Coulson A.,
RA Bonfield J., Burton J., Conneil M., Pavello A., Fraser A.,
RA Craxton M., Dear S., Du Z., Durbin R., Hawkins T., Hillier L., Jier M.,
RA Fultons L., Gardner A., Green P., Hawkes T., Laister N.,
RA Johnston L., Jones M., Kersey J., Kirsten J., Laister N.,
RA Latreille P., Lighthouse J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkhen R.,
RA Sims M., Smaldon N., Smith A., Smith M., Sonhammer E., Staden R.,
RA Sulston J., Thiermy-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA Wohldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
```


OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
OX NCBI_taxID=7159;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Koashiung;
RX MEDLINE=95333127; PubMed=7608924;
RA Ho C.M., Liu Y.M., Wei Y.H., Hu S.T.;
RT "Gene for cytochrome c oxidase subunit II in the mitochondrial DNA of
RL Culex quinquefasciatus and Aedes aegypti (Diptera: Culicidae).";
CC J. Med. Entomol. 32:174-180(1995).
CC -!- FUNCTION: Cytochrome c oxidase is the component of the respiratory
CC chain that catalyzes the reduction of oxygen to water. Subunits 1-
CC 3 form the functional core of the enzyme complex. Subunit 2
CC transfers the electrons from cytochrome c via its binuclear copper
CC A center to the bimetallic center of the catalytic subunit 1.
CC -!- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -!- COFACTOR: Copper A.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -!- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.
CC -----
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CC -----
DR EMBL; L34412; AAA79168.1; -.
DR HSP; P18400; ICYX.
DR InterPro; IPR001505; Copper_CuA.
DR InterPro; IPR008972; CupredOxin.
DR InterPro; IPR002429; Cyt_c_ox_2.
DR Pfam; PF00116; COX2; 1.
DR Pfam; PF02730; COX2; 1.
DR PRINTS; P01166; CYCOXIDASEII.
DR ProDom; PD000131; Copper_CuA; 1.
DR PROSITE; PS00078; COX2; 1.
KW Oxidoreductase; Copper; Mitochondrion; Transmembrane; Inner membrane;
KW Electron transport; Respiratory chain.
FT DOMAIN 1 26 MITOCHONDRIAL INTERMEMBRANE (POTENTIAL).
FT TRANSMEM 27 48 POTENTIAL.
FT DOMAIN 49 62 MITOCHONDRIAL MATRIX (POTENTIAL).
FT TRANSMEM 63 82 POTENTIAL.
FT DOMAIN 83 228 MITOCHONDRIAL INTERMEMBRANE (POTENTIAL).
FT METAL 161 161 COPPER A (PROBABLE).
FT METAL 196 196 COPPER A (PROBABLE).
FT METAL 200 200 COPPER A (PROBABLE).
FT METAL 204 204 COPPER A (PROBABLE).
SQ SEQUENCE 228 AA; 26491 MW; 0D69A2DCAA788789 CRC64;
Query Match 21.3%; Score 48.5; DB 1; Length 228;
Best Local Similarity 25.3%; Pred. No. 21;
Matches 20; Conservative 8; Mismatches 18; Indels 33; Gaps 3;
QY 1 MNGFASLLRRNQFILL-----VFLQLQISGLGIDISRP----- 34
Db 130 LMGFRLLVDVNRILPMNNQIRILVTATDVLSHTVPSLGKVIDATPGRLNQTNFLINQP 189
QY 35 -----TAEYC-ATHTISP 46
Db 190 GLPFGQCSEICGANHSFMP 208

Search completed: March 8, 2004, 12:12:06
Job time : 8.29515 secs

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OM protein - protein search, using sw model

Run on: March 8, 2004, 12:02:31 ; Search time 35.2599 Seconds

(without alignments)
411.624 Million cell updates/sec

Title: US-09-600-932-2_COPY_1_46

Perfect score: 228

Sequence: 1 MNGFASLRRNQFILLVFL.....GLDIDSRPTAEVCATHITSP 46

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL.25.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phage.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_virus.*

16: sp_bacteriaph.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	228	100.0	277	4	Q9V6Z7
2	162	71.1	277	11	Q8C1C5
3	159	68.7	277	11	Q8CF98
4	59	25.9	320	16	Q7V514
5	57	25.0	534	16	Q8E272
6	56.5	24.8	460	16	Q8F9X2
7	55.5	24.3	272	16	Q8DVX0
8	55	24.1	159	5	Q8I1B9
9	55	24.1	362	16	Q982I8
10	54.5	23.9	228	8	Q9B813
11	54	23.7	261	4	Q8NGX4
12	54	23.7	473	5	Q86JY9
13	54	23.7	1419	5	Q8IAX3
14	53.5	23.5	483	4	Q9V6V7
15	53.5	23.5	504	16	Q92KV3
16	53	23.2	268	4	Q9H670

17	53	23.2	304	4	Q9H079
18	53	23.2	339	5	Q8SW71
19	53	23.2	386	16	Q8YWS7
20	53	23.2	788	16	Q882Q7
21	52.5	23.0	173	2	O51892
22	52.5	23.0	228	8	O48399
23	52.5	23.0	228	8	O48312
24	52.5	23.0	228	8	O47820
25	52.5	23.0	228	8	O47822
26	52.5	23.0	228	8	O47818
27	52.5	23.0	228	8	O47821
28	52.5	23.0	228	8	O47819
29	52.5	23.0	228	8	O48360
30	52.5	23.0	228	8	O48323
31	52.5	23.0	228	8	O47823
32	52.5	23.0	228	8	O48283
33	52.5	23.0	597	16	O51037
34	52	22.8	137	2	O68055
35	52	22.8	162	4	O9NFI0
36	52	22.8	221	16	Q892S4
37	52	22.8	258	11	Q8BXG3
38	52	22.8	433	16	Q9PE45
39	52	22.8	433	16	Q87E54
40	52	22.8	435	5	Q9Y016
41	52	22.8	477	5	Q22532
42	52	22.8	562	11	Q8BXL9
43	52	22.8	794	5	Q9V4X7
44	52	22.8	794	5	O96648
45	52	22.8	820	5	Q9V4X6

ALIGNMENTS

RESULT 1

Q9V6Z7 PRELIMINARY; PRT; 277 AA.

AC Q9V6Z7; 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Collectin 34.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99240768; PubMed=10224141;
RA Ohtani K., Suzuki Y., Eda S., Kawai T., Kase T., Yamazaki H.,
Kashi H., Sakai Y., Fukuh A., Sakamoto T., Wakamiya N.;
RT "Molecular cloning of a novel collectin from liver (CL-L1).";
RL J. Biol. Chem. 274:13681-13689 (1999).
DR EMBL; AB002631; BAA81747.1; -;
DR HSSP; P19999; 2MSB.
DR Genew; HGNC:2220; COLEC10.
DR GO; GO:0005737; C:cytoplasm; TAS.
DR GO; GO:0005530; F:lectin; TAS.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF01391; Collagen; 1.
DR Pfam; PF00059; Lactin; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE LECTIN 1; 1.
DR PROSITE; PS00041; C-TYPE LECTIN 2; 1.
SQ SEQUENCE 277 AA; 30733 MW; 9736861CEBDC5C25 CRC64;

Query Match 100.0%; Score 228; DB 4; Length 277;
Best Local Similarity 100.0%; Pred.No. 3.5e-24;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MNGFASLRRNQFILLVFLFLQLQSLGLDIDSRPTAEVCATHITSP 46

RESULT 3	
ID	Q8CF98
QC	PRELIMINARY;
ID	Q8CF98 PRT; 277 AA.
AC	O8CF98;
DT	01-MAR-2003 (TREMELrel. 23, Created)
DT	01-MAR-2003 (TREMELrel. 23, Last sequence update)
DT	01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE	Collectin-L1.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
OX	NBGI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=C57BL 6J; TISSUE=Liver;
RX	MEDLINE=22333927; PubMed=12450124;
RA	Kawai T., Suzuki Y., Eda S., Kase T., Ohtani K., Sakai Y., Keshi H.,
RA	Fukuchi A., Sakamoto T., Noraki M., Copeland N.G., Jenkins N.A.,
RA	Wakamiya N.;
RT	"Molecular Cloning of Mouse Collectin Liver 1.";
RL	BioSci. Biotechnol. Biochem. 66:2134-2145(2002).
DR	ENBL; AB016429; BAC53954.1; -.
DR	GO; GO:0005529; F:sugar binding; IEA.
DR	InterPro; IPR008160; Collagen.
DR	InterPro; IPR001304; Lectin_C.
DR	Pfam; PF01391; Collagen; 1.
DR	Pfam; PF00059; lectin_c; 1.
DR	SMART; SM00034; CLECT; 1.
DR	PROSITE; PS00615; C TYPE LECTIN; 1.

```

RESULT 5
Q8EZ72 PRELIMINARY; PRT; 534 AA.
ID
AC Q8EZ72;
DT 01-VAR-2003 (TremBLrel. 23, Created)
DT 01-VAR-2003 (TremBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Transcriptional regulator, Arac family.
DS
GN IA3986.
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=173;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RC Ren S.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RA EMBL; AE011553; AA51184.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR00005; HTHArac.
DR Pfam; PF00165; HTH Arac; 1.
DR PRINTS; PR00032; HTHArac.
DR

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```
DR SMART; SM00342; HTH_ARAC; 1.
DR PROSITE; PS01124; HTH_ARAC_FAMILY_2; 1.
KW Complete proteome.
SQ SEQUENCE 534 AA; 62570 MW; 66CA1B43663172AB CRC64;

Query Match      25.0%; Score 57; DB 16; Length 534;
Best Local Similarity 44.8%; Pred. No. 17;
Matches 13; Conservative 5; Mismatches 9; Indels 2; Gaps 1;

QY 11 NQFILLVFLFQIQSLGDLIDSRPTAEVC 39
Db 14 NCFLFLILFLFSV--LSKEIHSSPVAETC 40

RESULT 6
Q8F9X2 PRELIMINARY; PRT; 460 AA.
AC Q8F9X2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE DNA-damage-inducible protein F.
EN DINF OR IA0065.
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
CX NCBI_TaxID=173;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RA Ren S.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE011198; AAN47264.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015297; F:antiporter activity; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0015238; F:drug transporter activity; IEA.
DR GO; GO:0004672; F:protein kinase activity; IEA.
DR GO; GO:0006855; F:multidrug transport; IEA.
DR GO; GO:0006488; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR002528; MateJ.
DR TIGRFAMs; TIGR00719; Prot_kinase.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
KW Complete proteome.
SQ SEQUENCE 460 AA; 51905 MW; D350920FAF098166 CRC64;

Query Match      24.8%; Score 56.5; DB 16; Length 460;
Best Local Similarity 37.8%; Pred. No. 17;
Matches 17; Conservative 8; Mismatches 19; Indels 1; Gaps 1;

ZY 1 MNGFASLLRRNQFLLVFLFQIQ-SLGLDIDSRPTAEVCATHYI 44
Db 245 VQGFSSLLHKNKDFLRTFFLIITFSIFRNFSSAAGTEILATNSI 289

RESULT 7
Q8DVKO PRELIMINARY; PRT; 272 AA.
AC Q8DVKO;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Conserved hypothetical protein.
EN SMU 485.
OS Streptococcus mutans.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.
CX NCBI_TaxID=11309;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UAI59 / ATCC 700610 / Serotype C;
RX MEDLINE=22295063; PubMed=12397186;
XA Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,

RA Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Qian Y.,
RA Li S., Zhu H., Najjar F., Lai H., White J., Roe B.A., Ferratti J.J.;
RT "Genome sequence of Streptococcus mutans UA159, a cariogenic dental
RT pathogen.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).
DR EMBL; AE014894; AAN58231.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 272 AA; 30940 MW; 376990BE23D7542F CRC64;

Query Match      24.3%; Score 55.5; DB 16; Length 272;
Best Local Similarity 35.3%; Pred. No. 14;
Matches 12; Conservative 8; Mismatches 9; Indels 5; Gaps 1;

QY 1 MNGFASLLRRNQFLLVFLFQIQSLGDLIDSRP 34
Db 125 INHFAQVKKRNYALLTL-----QEEGLDVTKKP 153

RESULT 8
Q8II89 PRELIMINARY; PRT; 159 AA.
AC Q8II89;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
EN PF11 0285.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
CX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RX MEDLINE=22255705; PubMed=12368864;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.-S., Nene V., Shallow S.J., Suh B., Peterson J., Angiuoli S.,
RA Perteira M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C., Venter J.C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrell B.;
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum.";
RL Nature 419:498-511(2002).
DR EMBL; AE014840; AAN35869.1; -.
KW Hypothetical protein.
SQ SEQUENCE 159 AA; 19472 MW; EFD2D84D2B298D00 CRC64;

Query Match      24.1%; Score 55; DB 5; Length 159;
Best Local Similarity 30.2%; Pred. No. 9.4;
Matches 13; Conservative 11; Mismatches 9; Indels 10; Gaps 2;

QY 8 LRENQFLLVFLFQIQSLGDLIDSRPTAEVC-----ATHYIS 45
Db 6 MKKNKFLFFFLFKTKVHIE-----TRKNCNVLFQFGTHAIT 43

RESULT 9
Q98E18 PRELIMINARY; PRT; 362 AA.
AC Q98E18;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Proline dipeptidase.
EN MLR4446.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
CX NCBI_TaxID=381;
RN [1]
```

GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0006118; F:electron transport; IEA.
GO; GO:0006810; F:transport; IEA.
InterPro; IPR001505; Copper_CuA.
InterPro; IPR008972; Cupredoxin.
InterPro; IPR002429; Cyt_c_ox_2.
Pfam; PF00116; COX2; 1.
Pfam; PF02790; COX2_TM; 1.
PRINTS; PR01166; CYCOXIDASEII.
ProDom; PD000131; Copper_CuA; 1.
PROSITE; PS00078; COX2; 1.
COPPE; Electron transport; Inner membrane; Membrane; Oxidoreductase;
Respiratory chain; Transmembrane; Transport; Mitochondrion.
NON_FT 228
SEQUENCE 228 AA; 26422 MW; D03013906959120F CRC64;

Query Match 23.9%; Score 54.5; DB 8; Length 228;
Best Local Similarity 26.8%; Pred.No.16; Matches 21; Conservative 8; Mismatches 17; Indels 33; Gaps 3;

QY 1 MNGFASLRRNQFILL-----VFLLQIQSLGIDISRP----- 34
DDB 130 LNGFRSLVDNRILPLNNQIRILVTATDVLHSTWVPSLGKVIDATPGRLNQTNLNQNS 189
QY 35 -----TAEVC-AATHISP 46
DDB 190 GLFPGQCSEICGANHSFMP 208

RESULT 11
Q8NGX4
ID Q8NGX4 PRELIMINARY; PRT; 261 AA.
AC Q8NGX4;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Seven transmembrane helix receptor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
SU Suwa M., Sato T., Okouchi I., Arita M., Putami K., Matsumoto S.,
TS Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RT Genome-wide discovery and analysis of human seven transmembrane helix
RT receptor genes";
RT Submitted (JUL-2001) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AB065642; BAC05868.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001594; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; F:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHRHODOPGN.
DR PROSITE; PS0262; G_PROTEIN_RECPE_F1_2; 1.
DR Receptor; Transmembrane.
KW Receptor; Transmembrane.
SQ SEQUENCE 261 AA; 29358 MW; 79950D2ED442A9E CRC64;

Query Match 23.7%; Score 54; DB 4; Length 261;
Best Local Similarity 25.0%; Pred.No.22; Matches 16; Conservative 9; Mismatches 19; Indels 20; Gaps 17;

QY 3 GFASLRRNQFILLVFLLQIQSLGIDISRP-----AEVCATH 42
DDB 16 GFSLARLQQLVFVLLYVLTFLGNALITIVLDRLHIPWYFFLAISCSEICYTF 75
QY 43 TISP 46
DDB 76 IIVP 79

```
RESULT 12
Q86JY9 Q86JY9 PRELIMINARY; PRT; 473 AA.
AC Q86JY9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to Dictyostelium discoideum (Slime mold). Ras-related protein
DE RAB.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RX MEDLINE=22092622; PubMed=12097910;
RA Goeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
RA Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
RA Tungal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
RT Nature 418:79-85(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RA Baumgart C.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC116984; RAO51356.1; -.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0003928; F:RAB small monomeric GTPase activity; IEA.
DR GO; GO:0003930; F:RAS small monomeric GTPase activity; IEA.
DR GO; GO:0003931; F:Rho small monomeric GTPase activity; IEA.
DR GO; GO:0015031; P:protein transport; IEA.
DR GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.
DR GO; GO:0000160; P:two-component signal transduction system (p. . .; IEA.
DR InterPro; IPR003579; GTPase_Rab.
DR InterPro; IPR003577; GTPase_Rab.
DR InterPro; IPR003578; GTPase_Rho.
DR InterPro; IPR01806; Ras transfrmg.
DR InterPro; IPR02078; Sig54 interact.
DR Pfam; PF00071; ras; 1.
DR PRINTS; PR00449; RASTNSFRMG.
DR SMART; SM00175; RAB; 1.
DR SMART; SM00173; RAS; 1.
DR SMART; SM00174; RHO; 1.
DR TIGRFAMs; TIGR00231; small GTP; 1.
DR PROSITE; PS00675; SIGMA54 INTERACT 1; 1.
SQ SEQUENCE 473 AA; 54662 MW; 6486F43077B5B73E CRC64;

Query Match 23.7%; Score 54; DB 5; Length 473;
Best Local Similarity 32.4%; Pred. No. 41;
Matches 11; Conservative 7; Mismatches 16; Indels 0; Gaps 0;

QY 11 NQFLLVFLQIQSLGDLDSRPTAEVCATHTI 44
DB 5 NLFILICFYINYSIGADRNFINEILAKSI 38

RESULT 13
Q81AX3 Q81AX3 PRELIMINARY; PRT; 1419 AA.
AC Q81AX3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN PF08_0078.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.

Query Match 23.5%; Score 53.5; DB 4; Length 483;
Best Local Similarity 28.6%; Pred. No. 1.3e+02;
Matches 10; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

QY 1 MNGFASLLRRNQFILLVFLQIQSLGDLDSRPT 35
DB 343 LNTLSSVKKNDFTLLYKILSYMKNGIELSLNPT 377

RESULT 14
Q9Y6V7 Q9Y6V7 PRELIMINARY; PRT; 483 AA.
ID Q9Y6V7;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DR R27090.2 (Hypothetical protein).
DE Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lamerdin J.E., McCready P.M., Adamson A.W., Burkhardt-Schultz K.,
RA Garcia E., Kyle A., Ramirez M., Stilwagen S., Garnes J., Dangauan L.,
RA Bruce R., Quan G., Montgomery M., Ow D., Kobayashi A., Olsen A.O.,
RA Carrano A.V.;
RT "Sequence analysis of an ~1 Mb region containing the MEF2B gene in
RT 19p13.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RA Strausberg K.;
CC -1- SIMILARITY: BELONGS TO THE DEAD BOX HELICASE FAMILY.
DR EMBL; AC002985; AAB81544.1; -.
DR EMBL; BC002674; AAH02674.1; -.
DR HSP; Q58083; 1HV8.
DR Genew; HGNC:18684; DDX49.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008026; F:ATP dependent helicase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR000629; DEAD_box.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
DR PROSITE; PS00039; DEAD ATP HELICASE; 1.
KW Hypothetical protein; ATP-Binding; Helicase; Hydrolase.
OX NCBI_TaxID=36329;
SQ SEQUENCE 483 AA; 54226 MW; 2B46DD6A992B2532 CRC64;

Query Match 23.5%; Score 53.5; DB 4; Length 483;
```

Best Local Similarity 35.9%; Pred. No. 49;
Matches 14; Conservative 5; Mismatches 17; Indels 3; Gaps 1;

QY 4 FASLLRNQFILLVFLQLQISLGIDSDSRPTAEVCATH 42
Db 288 FAALAKFKSIYRIILATDVASRGLDI---PTVQVINH 323

RESULT 15

Q92KV3 PRELIMINARY; PRT; 504 AA.
AC Q92KV3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein R00037.
GN R00037 OR SMC02757.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396507; PubMed=11481430;
RA Capela D., Barloy-Hubler F., Guzy J., Bothe G., Ampe F., Batut J.,
RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
RA Pohl T., Portetelle D., Puehler A., Furnelle B., Ramsperger U.,
RA Renard C., Thebault P., Vandenbol M., Weidner S., Gaibert F.,
RT "Analysis of the chromosome sequence of the legume symbiont
Sinorhizobium meliloti strain 1021.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
DR EMBL; AL591782; CAC41424.1; -.
DR InterPro; IPR003442; UPF0079.
DR Pfam; PF02367; UPF0079; 1.
DR TIGRFAMs; TIGR00150; TIGR00150; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 504 AA; 56713 MW; 255569A6CDADC0E CRC64;

Query Match 23.5%; Score 53.5; DB 16; Length 504;
Best Local Similarity 36.4%; Pred. No. 52;
Matches 16; Conservative 6; Mismatches 11; Indels 11; Gaps 2;

QY 5 ASILLRNQFILLVLP-----LLQISLG----LDIDSRPTAE 37
Db 228 SQLRRKGFAPIYARDLDQGLLIENLSEGLDIDGRPAE 271

Search completed: March 8, 2004, 12:15:10
Job time : 37.2599 secs

Use for Registration

GenCore version 5.1.6
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M protein - protein search, using sw model

un on: March 8, 2004, 12:03:01 ; Search time 12.1586 Seconds
(without alignments)
363.925 Million cell updates/sec

itle: US-09-600-932-2_COPY_1_46
erfect score: 228
equence: 1 MNGFASLLRNQFILLVFL.....GLDIDSRPTAEVCATHITSP 46

oring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

earched: 283366 seqs, 96191526 residues

otal number of hits satisfying chosen parameters: 283366

inimum DB seq length: 0
aximum DB seq length: 200000000
ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

atabase : PIR_78:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Match	Length	DB ID	Description
1	159	69.7	277	2 JC7903	collectin liver 1
2	53	23.2	386	2 AE1996	hypothetical prote
3	52.5	23.0	597	2 D70100	phosphoglucomutase
4	52	22.8	137	2 T03488	glutamate-tRNA lig
5	52	22.8	433	2 C82713	polysaccharide bio
6	51.5	22.6	155	2 C86206	hypothetical prote
7	51	22.4	157	2 AG2775	protein-export mem
8	51	22.4	162	2 E97555	hypothetical prote
9	51	22.4	328	2 H81996	probable integral
10	51	22.4	328	2 E81225	hypothetical prote
11	51	22.4	337	2 T28826	hypothetical prote
12	51	22.4	814	2 JC7389	thyroid stimulat
13	51	22.4	1077	2 T20579	hypothetical prote
14	50.5	22.1	332	2 C64073	rbp repressor homo
15	50.5	22.1	425	2 E70813	hypothetical prote
16	50	21.9	168	2 S73450	MG27 homolog B01
17	50	21.9	231	2 F89856	conserved hypothet
18	50	21.9	281	1 B47629	cell surface glyco
19	50	21.9	685	2 T12139	NADH2 dehydrogen
20	50	21.9	777	2 AC3273	cell division prot
21	50	21.9	1152	2 F86363	hypothetical prote
22	49.5	21.7	182	2 S40729	hypothetical prote
23	49	21.5	105	2 G71294	hypothetical prote
24	49	21.5	186	2 F86830	hypothetical prote
25	49	21.5	309	2 E71019	NADH2 dehydrogen
26	49	21.5	309	2 H75113	NADH2 dehydrogen
27	49	21.5	335	2 T16359	hypothetical prote
28	49	21.5	484	2 S36339	phosphorin II - V
29	49	21.5	488	2 T10794	phosphorin III -

ALIGNMENTS

RESULT 1

JC7903
collectin liver 1 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 03-Feb-2003 #sequence_revision 03-Feb-2003 #text_change 31-Mar-2003
C:Accession: JC7903
R:Kawai, T.; Suzuki, Y.; Eda, S.; Kase, T.; Ohtani, K.; Sakai, Y.; Keshi, H.; Fukuhara, A
Biochem. Biotechnol. Biochem. 66, 2134-2145, 2002
A:Title: Molecular cloning of mouse collectin liver 1.
A:Reference number: JC7903; MUID:22333927; PMID:12450124
A:Accession: JC7903
A:Molecule type: mRNA
A:Residues: 1-277 <KAW>
A:Cross-references: DDBJ:AB016429
A:Experimental source: liver
C:Comment: This protein is a highly conserved cytosolic protein and belongs to a vertebr
c development.
C:Genetics:
A:Gene: C111
A:Map position: 15

Query Match 69.7%; Score 159; DB 2; Length 277;
Best Local Similarity 71.7%; Pred. No. 1.9e-14; Indels 0; Gaps 0;
Matches 33; Conservative 3; Mismatches 10; 13

Qy 1 MNGFASLLRNQFILLVFLQLQSLGLDIDSRPTAEVCATHITSP 46
Db 1 MNGFVLLRSNLSMLLLALLHFLQSLGLDVDSRAAEVCATHITSP 46

RESULT 2

AE1996
hypothetical protein all1523 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C:Accession: AE1996
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AE1996
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-386 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA077889.1; PID:gl7135343; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all1523

Query Match 23.2%; Score 53; DB 2; Length 386;